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; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: HUMAN MAMMARY EPITHELIUM LIBRARY
; TITLE OF INVENTION: HUMAN MAMMARY EPITHELIUM LIBRARY
; FILE REFERENCE: 1600.1086.001
; CURRENT APPLICATION NUMBER: US/09/522,303
; CURRENT FILING DATE: 2000.03.08
; EARLIER APPLICATION NUMBER: 60/123,393
; BARLIER APPLICATION NUMBER: 60/123,393
; SOFUTARE: FALLS 1999.03.08
; SOFUTARE: FALLS OF WINDOWS VERSION 3.0
; SEQ ID NOS: 1353
; SEQ ID NO 1293
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; LOCATION: (1)...(4661)
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                                       NAME/KEY: misc feature;

LOCATION: (1).T.(4664);

OTHER INFORMATION: n = US-09-315-788A-1729
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
TITLE OF INVENTION: HUMAN ASTROCYTE LIBRARY
TITLE OF INVENTION: HUMAN ASTROCYTE LIBRARY
FILE REPERENCE: 1600.1019-002
CURRENT FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 09/315,788
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-22
PRIOR FILING DATE: 1999-05-22
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/132,067
PRIOR PLING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 2346
SEQ ID NO 1729
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Matches:
Conservative:
Mismatches:
Indels:
FILE REFERENCE: 1600.1019-002
CURRENT APPLICATION NUMBER: US/09/783,514
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 09/315,788
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-32
NUMBER OF SEQ ID NOS: 2346
SEQ ID NO 1729
LENGTH: 4664
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LOCATION: (1)....(4664);
OTHER INFORMATION: n =
US-09-783-514-1729
                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapien
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Query Match:
DB:
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6 rPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSe 53	536 rarghmeAlaserLeuGinFrovalSerAshGiniteGluargCyshanSerLeuAlarn 556	yleugluilemetileglyLysLysLysLyslloglnGlydleglnGlyHisTyrAsnSerCysTyrLe 596	596 uaspSerThrLeuPheCysLeuPhaAlaPheSerSerValLeuAspThrValLeuLeuAr. 616 	31uTP	636 ulleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuAr 656 	656 gLyg1leLeuGluLygValGluAlaAlaSerGlyPheThrSerGluGluLygAspProGl 676	heHisHisIleLeuargValGluProLeuLeuLy 	696 gSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGl 716 	JGJUTrpSerPhelleAsnSerPhelleAsnSerPhelleAshSerPhelle	736 uLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPh 756	eProSerLeuGluLe 	776 pThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTy 796	796 rAspAspProAsp11eSerAlaGlyLys11eLysGlnPheCysLysThrCysAsnThrCl 816 	816 nValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAs 836	836 pLeubroAspIrpAspIrpArgHisGlyCysIleProCysGlnAsnMetGluleuPheAl 856	856 aValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSe 876
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Sequence 4309, Application US/09396087

SEQUENCE 4309, Application US/09396087

APPLICANT: Gearing, David P.

APPLICANT: Holtzman, Douglas A.

TITLE OF INVENTION: PULMONARY ARTERY SMOOTH MUSCLE LIBRARY

TITLE OF INVENTION: PULMONARY ARTERY SMOOTH MUSCLE LIBRARY

CURRENT APPLICATION NUMBER: 05/09/396,087

CURRENT FILING DATE: 1999-09-14

EARLIER FILING DATE: 1998-09-14

EARLIER FILING DATE: 1998-09-14

EARLIER FILING DATE: 1998-09-14

EARLIER PLICATION NUMBER: 60/100,266

EARLIER APPLICATION NUMBER: 60/107,226

EARLIER APPLICATION NUMBER: 60/110,65

EARLIER PLING DATE: 1999-04-30

NUMBER OF SEQ ID NOS: 5220

SOFTWARE FEALOR DATE: 1999-04-30

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FRATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4668)
; OTHER INFORMATION: n = A
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CURRENT APPLICATION NUMBER: US/09/432,241A
CURRENT FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/106,445
PRIOR APPLICATION NUMBER: 60/107,227
PRIOR APPLICATION NUMBER: 60/107,227
PRIOR APPLICATION NUMBER: 60/107,227
PRIOR APPLICATION NUMBER: 60/127,182
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 5041
SOFTWARE: FEARESEQ FOR WINDOWS VERSION 3.0
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; GENERAL INFORMATION:
    APPLICANT: Gearing, David P.
    APPLICANT: Holtzman, Douglas A.
    TITLE OF INVENTION: HUMAN EPIDERMAL KERATINOCYTE LIBRARY
    FILE REFERENCE: 1600.1004001
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                                                             830 AAGCTAGAACTCATAGAAGATGATGACACTGCATTGGAAAGTGATTACGCAGGTCCTGGG
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                                                                                                  Sequence 1278, Application US/09434737

GENERAL INFORMATION:
APPLICANT: Gearing, David P.
TITLE OF INVENTION: HUMAN MIXED LYMPHOCYTE LIB
FILE REFERENCE: 1600.1067001
CURRENT FILING DATE: 1999-11-05
EARLIER FILING DATE: 1999-11-05
EARLIER FILING DATE: 1999-11-05
SOFTWARE PRING DATE: 1999-11-05
SOFTWARE PRING DATE: 1999-11-05
SOFTWARE PRING DATE: 1999-11-05
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; LOCATION: (1)...(4668)
; CTHER INFORMATION: n = A,T,C
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ORGANISM: Homo sapiens
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Percent Similarity;
Best Local Similarity:
Query Match:
DB:
                                                                          RESULT 12
US-09-434-737-1278
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Pred. No.:
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Sequence 1279, Application US/09850118
Sequence 1279, Application US/09850118
Sequence 1270, Application David P.
TITLE OF INVENTION: MUCLEIC ACID MOLECULES DERIVED FROM A TITLE OF INVENTION: MUCLEIC ACID MOLECULES DERIVED FROM A TITLE OF INVENTION: MUCLEIC ACID MOLECULES DERIVED FROM A TITLE OF INVENTION: MUCLEIC ACID MOLECULES DERIVED FROM A TITLE OF INVENTION: MUCHER: 105/09/850,118
CURRENT APPLICATION NUMBER: US 60/107,228
PRIOR PILING DATE: 1998-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 1830
SOFTWARE: FastSEQ for Windows Version 4.0
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3049 TATGTGCATGTACCAGAGTCCAACAATGAGTTTGTACAAA 3088
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US-09-850-118-1278
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Best Local Similarity:
Query Match:
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ORGANISM: HOMO
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US-09-850-118-1278
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uGluPheLeuAsnIleLeuPheHisHisIleLeuArgValGluProLeuLysIleAr
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        pThrProArgGlnCysArg1leCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTy

                                               yLeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLe
                                                                                                                                                                                                                      uAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuAr
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                                                                                           eGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGl
                                                                                                                                                                                                                                                                                      gProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGl
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Oy 476 OPheTyrGlyValileArgTrplleGlyGlnProProGlyLeuAsnGluValLeuAlagl 496			2089 ACCCAAAGAAAGAACGATGTAGAATATTATAGTGAAACCCAAGAGCTACTGAGGACAGA 2160 UllevalAsnProleuArglleTyrGlyTyrvalCysAlaThrLys1leMetLysLeuAr 6511	Qy 656 gLysIleLeuGluLysValGluAlaAlaSerGlyPheThrSerGluGluLysAspProGl 676 Db 2209 GAAATACTTGAAAAGGTGGAGGCTGCATCAGGATTACCTCTGAAGAAAAAGATCTGTGA 226 Qy 676 uGluPheLeuAsnIleLeuPheHisHisIleLeuArgValGluProLeuLysIleAr 696 Db 2269 GGAATTCTTGAATATTCATGTTTCATATTTAAGGGTAGAACCTTTGCTAAAAATAAG 232	Qy 696 gSerAlaGlyGlnLygValGlnAspCysTyrPheTyrGlnIlePheMetGluLygAsnGl 716	2389 GAAGTTGCCGTTCTCACAGTTGTTTGTTAGATGGTCTTTTATCACAGTAACCT 24 736 ULYSPHAAlaGIUAlaProSerCYGLeuIleIleGlnMetProArgHeGlyLySASPP 75 2449 GAAATTTGCAGAGCACCATCATGTCTGATTATCAGATGCTCTTTTATCAACAGTAACCT 24	Qy 756 eLysLeuPheLysLysIlePheProSerLeuGluLeudsnileThrAspLeuLeuGluAs 776 Db 2509 TAAACTATTAAAAATTTTCCTTCTCTGGAATTAAATATAACAGATTTACTTGAAGA 256 Qy 776 pThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTY 796 Db 2569 CACTCCCAGACAGTGCCGGATATGTGGAGGGCTTGCAATGTATGAGTGTAGAGAATGCTA 262	Oy 796 rAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGl 816
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456 OProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPr 476	536 rargPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPh 556 3204 TAGGTTTGCATCATTGCAGCGGTTTCCAATCAGTTGAGCGTTGTAACTCTTTAGCATT 3205 eGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGl 574 3264 TGGAGGCTACTTAAGTGAAGTAGAAAAATCTCCACCACAAAATGGAAAAAGAAGG 33: 576 yLeuGluIleMetIleGlyLysLysElysGlyIleGlnGlyHisTyrAsnSerCysTyrLe 594 3324 CTTGCAGATAATGATAAAAAAAAAAAAACGAAACTCAAAAAAAA	596 waspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuAr 611	676 uGluPheLeuAsnileLeuPheHisHislieleuArgValGluProLeuLeuLysileAr 69	Oy 736 uLysPhealaGlualaProSerCysLeulleIleGlnMetProArgPheGlyLysAspPh 756

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                         816 NValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSsrLeuProLysAs
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Search completed: April 17, 2005, 13:44:38 Job time : 7279 secs

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APPLICANT: Derry, Jonathan
APPLICANT: Panslow, William
APPLICANT: Dougall, William
APPLICANT: Dougall, William
TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING
FILE REFERENCE: 3198
CURRENT APPLICATION NUMBER: US/10/760,678
CURRENT FILING DATE: 2004-01-20
PRIOR APPLICATION WHOBER: US/09/851,673
PRIOR APPLICATE: 2001-05-08
NUMBER OF SEQ ID NOS: 4
            Sequence 114267,
Sequence 75550, A
Sequence 17891, A
Sequence 58260, A
Sequence 1731, Ap
Sequence 5500, Ap
                                                                                                                                                             Sequence 105317, Sequence 105317, Sequence 1033757, Sequence 1033757, Sequence 15680, App Sequence 15680, A Sequence 97836, A Sequence 45370, A Sequence 45370, A Sequence 45371, A Sequence 2961, App Sequence 5261, App Sequence 533, App Sequence 533, App Sequence 109221, Sequence 109221, Sequence 109221, Sequence 109221, Sequence 109221, Sequence 109221, Sequence 10921, A Sequence 109221, Sequence 10921, A Sequence 10921, A Sequence 10921, A Sequence 10921, A Sequence 109301, Sequence 109301, Sequence 109301, Sequence 1798, App Sequence 179
                                                                                                                                              Sequence 956, App
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Best Local Similarity:
Query Match:
  NAME/KEY: CDS
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LENGTH: 5371
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-MODEL=frame+ p2n.model -DEV=xlp
-G-/6cgdZ 1/087P0-gpool_PUS09671687/runat 15042005_163040_12041/app_query.fasta_1.1095
-DB=Pending_Patente NA, New -OFMT=fastap -SUFFIX=015go.rnpn -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=o1igo
-LOOPEXT=0 -UOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=01igo
-ALIGN=15 -MODE=LCOA1 -OUTPWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09671687_@CGN 1 1 268 @runat 15042005_163040_12041
-MATRIX=15 -MODE=LCOA1 -OUTPWT=pto -NORM=ext -NEG SCORES=0 -WAIT_ -DSPSDLCCK=100
-LOONG-1 -NORMENT -NEG SCORES=0 -WAIT_ -DSPSDLCCK=100
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Sequence 290, App
Sequence 26328, A
Sequence 20538, A
Sequence 20539, A
Sequence 20540, A
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2489.941 Million cell updates/sec
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1 MSSGLWSOEKVTSPYWEERI.....RLLCDAYMCMYQSPTWSLYK 949
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                                                                                                                                            April 17, 2005, 07:25:28 ; Search time 590 Seconds
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                   nucleic search, using frame_plus_p2n model
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US-10-122-851-290
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2049 TCCAGGAGAATCCAAGGCTGTGCACGAAGACTGCTTTGTGATGCATATATGTGCATGTAC 2108
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OTHER INFORMATION: 96% homologous to Homo sapiens Familial Cylindromatosis
COTHER INFORMATION: Gene, accession number AJ250014, Smith-Waterman Score=963.
US-10-450-763-26328
921 SerArgArgIleGInGlyCysAlaArgArgLeuLeuCysAspAlaTyrMetCysMetTyr 940
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                            TITLE OF INVENTION: 1999, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POL
FILE REPERENCE: 190CTP3/US
CURRENT PAPLICATION NUMBER: US/10/450,763
CURRENT PILING DATE: 2003-06-11
PRIOR PILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
                                                                 2109 CAGAGTCCAACAATGAGTTTGTACAAA 2135
                                                941 GlnSerProThrMetSerLeuTyrLys 949
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GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: ROSENFELD, David
                                                                                               RESULT 3
US-10-450-763-26328/c
; Sequence 26328, Application US/10450763
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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APPLICANT: MIT GENOMICS, INC.
APPLICANT: BAINGE, Sue K.
APPLICANT: ROSENFELD, David
APPLICANT: RERR, ALCHARI
APPLICANT: RERR, ALCHARI
APPLICANT: BATES, Stephen
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tow
TITLE OF INVENTION: METHODE & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEI
TITLE OF INVENTION: LIVESTOCK
FILE REFERENCE: MMI110-2
CURRENT APPLICATION WUMBER: US/10/972,079
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 60/514,333
PRIOR APPLICATION NUMBER: US 60/514,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NAI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: DeNISE, Sue K.
APPLICANT: BENEELD, David
APPLICANT: RERR, Richard
APPLICANT: BATES, Stephen
APPLICANT: HOLM, Tom
TITLE OF INVENTION: LIVESTOCK
TITLE OF INVENTION: LIVESTOCK
FILE REFERENCE: MANAGE NON-BEE!
CURRENT APPLICATION NUMBER: US/10/972,079
CURRENT FILING DATE: 2004-10-22
329 AAAAATGAGAAAGTTGGAGTCCCGACAATYCAGCAGTTACTGGAGTGGTCCTTCATCAAC 270
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PRIOR FILING DATE: 2003-10-24
NUMBER OF SEQ ID NOS: 96631
SEQ ID NO 19097
LENGTH: 600
                                                                                                                                                                 ; Sequence 20540, Application US/10972079; GENERAL INFORMATION:
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; ORGANISM: Chicken 19866894228522_1
US-10-972-079-19097
                                          734 SerAsnLeuLysPheAlaGlu
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SOFTWARE: Patentin version 3.1
SEQ ID NO 20540
LENGTH: 600
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US-10-972-079-20540/c
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GENERAL INFORMATION:
APPLICANT: MI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: RERR, Richard
APPLICANT: RERR, Richard
APPLICANT: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
TITLE OF INVENTION: LIVESTOCK
FILE REFERENCE: MAILLILO-2
CURRENT APPLICATION NUMBER: US/10/972,079
CURRENT APPLICATION NUMBER: US 60/514,333
PRIOR FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 60/514,333
            APPLICANT: BATES, Stephen
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
TITLE OF INVENTION: LIVESTOCK
FILE REFERENCE: MAI1110-2
CURRENT APPLICATION NUMBER: US/10/972,079
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 60/514,333
PRIOR FILING DATE: 2003-10-24
NUMBER OF SEQ ID NOS: 96631
SOFTWARE: PARCHELIN VERSION 3.1
SEQ ID NO 20538
LENGTH: 600
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US-10-972-079-20539
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SOFTWARE: PatentIN version 3.1
SEQ ID NO 20539
LENGTH: 600
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  KERR, Richard
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TYPE: DNA
ORGANISM: Heterodera glycines
ORGANISM: Heterodera glycines
ORGANISM: Location=4308..616
OTHER INFORMATION: Strand=+
OTHER INFORMATION: Strand=+
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Gene Ontology: Mol. function=heat shock protein activity; Cellula; OTHER INFORMATION: component=cytosol; Biological process=protein folding US-60-655-875-75550
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APPLICANT: Du, Zijing
APPLICANT: Du, Zijing
APPLICANT: Bou, Liang
APPLICANT: Gu, Zijing
APPLICANT: Gu, Maolong
APPLICANT: Lu, Maolong
APPLICANT: Miller, Nancy
APPLICANT: Miller, Nancy
APPLICANT: Williams, Deryck
APPLICANT: Wuldin, Mark
APPLICANT: Vaudin, Mark
APPLICANT: Wuldin, Mark
APPLICANT: Si - 21 (53885)
CURRENT APPLICATION NUMBER: US/60/655,875
CURRENT FILING DATE: 2005-02-24
NUMBER OF SEQ ID NOS: 171306
SEQ ID NO 17891
LENGTH: 2900
IN PLANTS AND COMPOSITIONS THEREOF
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               FILE REFERENCE: 38-21(53885)
CURRENT APPLICATION NUMBER: US/60/655,875
CURRENT FILING DATE: 2005-02-24
NUMBER OF SEQ ID NOS: 171306
LENGTH: 1854
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US-60-655-875-114267
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APPLICANT: Guo, Liang

APPLICANT: Kovalic, David

APPLICANT: Malong

APPLICANT: Miller, Nancy

APPLICANT: Williams, Deryck

CURRENT FILING DATE: 2005-02-24

NUMBER OF SEQ ID NOS: 171306

SEQ ID NOS: 171306

TYPE: NUMBER OF TARRETT APPLICANT

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TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
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ORGANISM: Heterodera glycines
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Guo, Liang
Kovalic, David
Lu, Maolong
McCarter, James
Miller, Nancy
Williams, Deryck
Vaudin, Mark
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                                                                                                            Percent Similarity:
Best Local Similarity:
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                           Alignment Scores:
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APPLICANT: Williams, Deryck
APPLICANT: Vaudin, Mark
APPLICANT: Vaudin, Mark
APPLICANT: Vaudin, Mark
APPLICANT: Wa, Wei
TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
FILE REFERENCE: 38-21(53885)
CURRENT APPLICATION NUMBER: US/60/655,875
CURRENT BILING DATE: 2005-02-24
NUMBER OF SEQ ID NOS: 171306
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TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: RHEWMATOID ARTHRITIS
FILE REPERENCE: 10872.514696
CURRENT APPLICATION NUMBER: US/10/287,436A
CURRENT FILING DATE: 2002-10-31
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; Sequence 956, Application US/10287436A
; GENERAL INFORMATION:
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NAME/KEY: misc_feature
LOCATION: (6672) ..(6672)
OTHER INFORMATION: n is a, c, g,
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                        ORGANISM: Heterodera glycines
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McCarter, James
Miller, Nancy
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Kovalic, David
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US-60-655-875-1731
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OTHER INFORMATION: SCN-specific regions: Sequence locations=1-298,343-353,376-457,48
OTHER INFORMATION: -804,826-991,1013-1382,1404-1630,1662-1822,1844-1871,1893-2224,22
OTHER INFORMATION: -2315,2337-2458,2483-2578,2600-2758,2780-2942,2964-3670,3693-3949
FEATURE:
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Cellular component=mitochondrial ribosome; Biological process
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                                                                                                                                                                                                                       APPLICANT: LA, Maclong
APPLICANT: LA, Maclong
APPLICANT: Malliams, Deryck
APPLICANT: Williams, Deryck
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; GENERAL INFORMATION:
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OTHER INFORMATION: Cellular compor;
OTHER INFORMATION: =gametogenesis
US-60-655-875-58260
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ORGANISM: Heterodera glycines
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Kovalic, David
Lu, Maolong
McCarter, James
Miller, Nancy
Williams, Deryck
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APPLICANT: Boukharov, Andrey
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OTHER INFORMATION: Strand=+
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Kovalic, David
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RESULT 15
US-11-036-317-90968
; Sequence 90568, Application US/11036317
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Williams, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REPERRUCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-50-1.3
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 90968
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                             NUMBER OF SEQ ID NOS: 1446
SOFTHARRE: FattSEQ for Windows Version 4.0
SEQ ID NO 956
LENGTH: 149034
PRIOR APPLICATION NUMBER: US 60/336,220 PRIOR FILING DATE: 2001-10-31
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Job time : 719 secs
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ORGANISM: Homo sapiens
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; Patent No. 6569662
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Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
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    US-09-620-312D-290
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Sequence 20085, A
Sequence 246, App
Sequence 216, App
Sequence 21, Appl
Sequence 219, App
Sequence 2194, Ap
Sequence 52159, A
Sequence 52159, A
Sequence 52159, A
Sequence 52159, A
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seg:*
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6: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seg:*
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US-09-134-001C-2194
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; ORGANISM: Homo s; PEATURE: NAME/KEY: CDS; LOCATION: (81)... US-09-620-312D-290
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FILE REFERENCE: 59.US2.REG CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT APPLICATION NUMBER: US 60/122,487
PRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 20085
LENGTH: 110
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APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Mohr, Christine
APPLICANT: Knechtle, Philipp
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           615 LeuArgProLysGluLysAsnAspValGluTyrTyrSerGluThrGln 630
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36
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: No. 6239264artis Corporation STRET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                         ; Sequence 20085, Application US/09513999C
; Patent No. 6783961
; GRNEAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-08-998-416-246/c
; Sequence 246, Application US/08998416
; Patent No. 6239264
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36.00
100.00%
100.00%
3.79%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-20085
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APPLICANT: Philip
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Best Local Similarity:
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US-09-513-999C-20085
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                     527
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DB:
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                                                                                                                                                       Sequence 3, Application US/09646403

Sequence 3, Application US/09646403

Patent No. 6734174

GENERAL INFORMATION:

APPLICANT: WALLACH, David

APPLICANT: WALLACH, David

APPLICANT: WALLACH, David

TITLE OF INVENTION: MODITHER PROTEINS

TITLE OF INVENTION: MODITHER PROTEINS

TITLE OF INVENTION: MODITHER PROTEINS

FILE REFERENCE: WALLACH=27

CURRENT FILING DATE: 1090-09-18

PRIOR APPLICATION NUMBER: 1C/1L99/00158

PRIOR FILING DATE: 1999-03-18

PRIOR FILING DATE: 1999-03-18

PRIOR FILING DATE: 1999-09-01

NUMBER OF SEQ ID NOS: 8

SOPTWARE: PatentIn version 3.1
2049 TCCAGGAGAATCCAAGGCTGTGCACGAAGACTGCTTTGTGATGCATATATGTGCATGTAC 2108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            407 AsnArgPheHisSerLeuProPheSerLeuThrLysMetProAsnThrAsnGlySerIle 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyHisSerProLeuSerLeuSerAlaGlnSerValMetGluGluLeuAsnThrAlaPro 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375 ACGGATGGAACCTTCAGAGGCACTCGGTATTTCACCTGTGCCCTGAAGAGGCGCTGTTT 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 AspPheAspArgSerSerProProLeuGlnProProProValAsnSerLeuThrThrGlu 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 GGCCACAGTCCACTTTCTCTGTCAGCCCAGTCTGTAATGGAAGAGCTAAACACTGCACCC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 GTCCAAGAGAGTCCACCCTTGGCCATGCCTCCTGGGAACTCACATGGTCTAGAAGTGGCC 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerLeuAlaGluValLysGluAsnProProPheTyrGlyValIleArgTrpIleGlyGln 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 TCATTGGCTGAAGTTAAGGAGAACCCTCCTTTCTATGGGGTAATCCGTTGGATCGGTCAG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315 CCACCAGGACTGAATGAAGTGCTCGCTGGACTGGAACTGGAAGATGAGTGTGTGCAGGCTGT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrAspGlyThrPheArgGlyThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPhe 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
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178
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Conservative:
Mismatches:
Indels:
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                                                           2109 CAGAGTCCAACAATGAGTTTGTACAAA 2135
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                                        941 GlnSerProThrMetSerLeuTyrLys
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i LOCATION: (691)..(691)
i OTHER INFORMATION: n is unknown.
US-09-646-403-3
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165.00
99.44%
99.44%
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ORGANISM: Homo sapiens
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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LENGTH: 2116
                                                                                                                                            US-09-646-403-3
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Patent No. 6444799
CENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLECTIDES AND USES THEREOF CORRESPONDENCE ADDRESS:
ADDRESSED: ADDRESS:
ADDRESSED: 755 PAGE MILL ROAD
Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-671-687A-3 (1-949) x US-08-998-416-246 (1-747)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
OPERATING SYSTEM: Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches:
Indels:
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30-JAN-1998
                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP11:
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP15:
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100.00%
0.95%
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COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                          ORGANISM: PAG1220RP
                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: CA
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-221-017B-1097
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US-09-526-193A-21

Sequence 21, Application US/09526193A

Patent No. 6617122

GENERAL INFORMATION:
APPLICANT: Hayden, Michael R.
APPLICANT: Brooks-Wilson, Angela R.
APPLICANT: Pimstone, Simon N.
TITLE OF INVENTION: CHOLESTEROL LEVELS
FILE REFERENCE: 50110/002005
CURRENT APPLICATION NUMBER: US/09/526,193A

CURRENT FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 60/124,702
PRIOR FILING DATE: 1999-06-08
PRIOR FILING DATE: 1999-06-08

PRIOR FILING DATE: 1999-06-17

PRIOR PILING DATE: 1999-06-17

PRIOR PILING DATE: 1999-09-01

NUMBER OF SEQ ID NOS: 287

SOFTWARE FRALSEQ for Windows Version 4.0
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                     TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1097:
SEQUENCE CHARACTERISTICS:
LENGTH: 6574 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                            NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 2734
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
JMBER: PP2911
09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: 1...6574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
  APPLICATION NUMBER
FILING DATE: 09-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
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US-09-221-017B-1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
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Pred. No.:
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVERTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: us,0409,949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,768
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PLILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 240, Application US/09232785

Patent No. 6733965

GENERAL INFORMATION:
APPLICANT: Enternational Paper Co.
APPLICANT: Enternational Paper Co.
APPLICANT: Bolson, C. Dana
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 4481/1E188US1
CURRENT APPLICATION NUMBER: US/09/232,785
CURRENT FILING DATE: 1999-01-15
PRIOR FILING DATE: 1999-01-15
PRIOR FILING DATE: 1999-01-15
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 397
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                               731 PhelleAsnSerAsnLeuLysPhe 738
                                                                                                                                                                                                                                                                                                                                                      180 TTCATTAACAGCAATTTGAAATTT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       649 AlaThrLysileMetLysLeuArg 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 GCGACAAGATTATGAAACTGAGA 15
                    LENGTH: 255
TYPE: DNA
TYPE: DNA
GGANISM: Staphylococcus epidermidis
US-09-134-001C-2194
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Best Local Similarity:
Query Match:
                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-949-016-52259
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US-09-232-785-240/c
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                                                                                                                             Alignment Scores:
  ; SEQ ID NO 2194
; LENGTH: 255
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LENGTH: 266
                                                                                                                                             Pred. No.:
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APPLICANT: LYAIN DOUGET CE ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCCUS TITLE OF INVENTION: NUCLEIC ACID AND PAMINO STICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-08-14
PRIOR PAPLICATION NUMBER: US 60/055,779
PRIOR PAPLICATION NUMBER: US 60/055,779
PRIOR PAPLICATION NUMBER: US 60/055,779
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                           ## APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-0-03

PRIOR PILING DATE: 2000-0-0-03

NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER: OF SEQ ID NOS: 207012

SEQ ID NO 12572

LENGTH: 53806
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; Sequence 12572, Application US/09949016
; Patent No. 6812339
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; Sequence 2194, Application US/09134001C
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i OTHER INFORMATION: n = a, t, c,
US-09-526-193A-21
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Best Local Similarity:
Query Match:
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ORGANISM: Human
                                                                                                                                             Percent Similarity:
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                                                                                   Alignment Scores:
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APPLICANT: VENTER, J. Craig et al
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ORGANISM: Human
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Sequence 52319, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: FastSEQ for Windows Version 4.0

SEQ ID NO 52319
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| Sequence 52320, Application US/09949016
| Patent No. 6812339
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| FILE REFERENCE: CL001307
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Matches:
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Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 52259
LENGTH: 601
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CURRENT FILING DATE: 2000-04-14
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Query Match:
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Best Local Similarity:
Query Match:
                                                                                                    TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
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WEACULT TO SEQUENCE 52321/C

### SEQUENCE 52321/C

### SEQUENCE 52321/C

### SEQUENCE 52321/C

### SEQUENCE 52321, Application US/09949016

### SEGUENCE NO. 6812339

### SEGUENCE NO. 6812339

### SEGUENCE NO. 6812339

### TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

### TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

### CURRENT PILING DATE: 2000-04-14

### PRIOR PLICATION NUMBER: 60/231,768

### PRIOR PLILING DATE: 2000-10-03

### PRIOR APPLICATION NUMBER: 60/231,498

### PRIOR PLILING DATE: 2000-10-03

### PRIOR PLILING DATE: 2000-10
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Matches:
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NOS: 207012
SEQ ID NO 52320
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; Sequence 56429, Application US/09949016

; Patent No. 681233

; GENERAL INFORMATION:
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Best Local Similarity:
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Search completed: April 17, 2005, 11:43:59
Job time: 429 secs

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RESULT 15

US-09-949-016-56450/c

Sequence 56450, Application US/09949016

Patent No. 691239

GENERAL INFORMATION:
PAPLICANT: UPENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION NUMBER: US/09/949,016

CURRENT PELING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE; PRESEQ FOR WINGOWS VERSION 4.0

SEQ ID NO 56450
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PELLORION NUMBER: 60/241,755
PRIOR PELLORION NUMBER: 60/241,755
PRIOR PELLORION NUMBER: 60/241,756
PRIOR PELLORION NUMBER: 60/237,768
PRIOR PELLORION NUMBER: 60/237,768
PRIOR PELLORION NUMBER: 60/237,498
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
SOFTWARE: FREESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 56429
LENGTH: 601
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Best Local Similarity:
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; ORGANISM: Human
US-09-949-016-56429
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ORGANISM: Human
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"Draft sequence of the Giardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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NCBI_TaxID=184922;
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0.8%; Score 8; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                    PIR; $6596; $6596.

Subtilier; BG10030; yyba.
InterPro; IPR000835; HTH Fis.
InterPro; IPR000835; HTH Mark.
InterPro; IPR000835; HTH Mark.
InterPro; IPR009989; Wing_hlx_DNa_bnd.
Pfam; PF01047; Mark; 1.
PRINTS; PR005999; HTHMARR; 1.
ITGRRAMs; ITGR01199; HTH fis; 1.
PROSITE; PS0117; HTH MARR; 1; 1.
PROSITE; PS0117; HTH MARR 1; 1.
PROSITE; PS0117; HTH MARR 2; 1.
I PROSITE; PS01995; HTH MARR 2; 1.
I PROSITE; PS01995; HTH MARR 2; 1.
I PROSITE; PS01991; HTH MARR 1; 1.
I PROMAIN 1 TABRECTIPTION FEGULATION.
I TABRECTIPTION FEGULATION.
I HTH MARR-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN 1 133 HTH mark-type.
SEQUENCE 150 AA; 17584 MW; E9195BBAD02DF4DC CRC64;
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EMBL, AACB010000050; EAA40124.1; -.
SEQUENCE 212 AA; 24313 MW; BCE7494F74925675 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               070716;
01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
GLP 80 31039 31677
Glardia lamblia ATC 50803
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                                    EMBL; D26185; BAA05202.1; -. EMBL; Z99124; CAB16108.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 SGFTSEEK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         666 SGFTSEEK 673
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Search completed: April 18, 2005, 09:40:35 Job time: 70 secs

103 ALDKLELI 110

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Pred. No.

100.0%;

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Klenk H.-P.;
"The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium from permanently of Arctic sediments.";
Environ. Microbiol. 61.887-902(2004).
EMBL; CR522870; CAG35490.1;
CG0; G0:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
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MEDLINE=22354719; PubMed=12466555; DOI=10.1093/nar/gkf667;
Sasaki Y., Ishikawa J., Yamashita A., Oshina K., Kenri T., Furuya K.,
Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma penetrans, an
intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M., Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K., Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
                                                                                                                                                                                                         OrderedLocusNames=DP0761;
Desulfotales psychrophila.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
Desulfobulbaceae; Desulfotalea.
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=28227;
                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Related to xylene monooxygenase electron transfer component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 225;
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100.0%; Pred. No. 4.7;
                                                         225 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001834; Cyt_B5_reductase.
InterPro; IPR001709; FPN cyt_redctse.
InterPro; IPR001433; Oxred_FAD/NAD(P).
InterPro; IPR001221; Phe hydroxylase.
Pfam; PF00175; NAD_binding_1; 1.
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                                                                                                                     Created)
                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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PRINTS; PR00410; PHEHYDRXLASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=LSv54 / DSM 12343;
PubMed=15305914;
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Best Local Similarity 100...
9, Conservative
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                                                         PRELIMINARY;
                                                                                                               (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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SEQUENCE 225 AA;
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25-OCT-2004
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RX KURDINE-90444033; PubMed=9384377; DOI=10.1038/36/86;

RX KUNST F., Ogasawara N., Moszer I., Albertini A.M., Bloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Bourschier L., Brans A., Braun M., Brignell S.C., Bron S.,
Broullet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Broullet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Brois S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Britan K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
Britan K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
A Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A Hilbert H., Holsappel S., Hosono S., Halech J., Harwood C.R., Henaut A.,
A Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
A Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
RA A Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
RA Bazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
Schin B.S., Soldo B., Sorokin A., Tanake B., Takagi T., Tarkahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Yamane K.,
Wassarotti A., Vlari A., Winters P., Wipat A., Yamamoto H., Yamane K.,
Wastarotti A., Vlari A., Wambutt R., Yamamoto H., Yamane K.,
Wastarotti A., Vlari A., Wanbutt R., Yamamoto H., Yamane K.,
Wastarotti A., Parek K., Yoshida K., Yoshikawa H.F., Zumstein B.,
The complete genome sequence of the Gram-positive bacterium Bacillus
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                         Indels
                                                                                                                                                                                                                                                                                          01-OCT-1994 (Rel. 30, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Putative HTH-type transcriptional regulator yybA.
Name-yybA; OrderedLocusNames=BSU40710;
Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillusceae; Bacillus.
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                         Mismatches
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or send an email to license@isb-sib.ch).
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                         8; Conservative
                                                                                                                                                                                                                                  STANDARD;
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                                                                      197 LDKLELIE 204
Best Local Similarity
Matches 8; Conserv
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                                                                                                              32 LOKLELIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1423;
                                                                                                                                                                                                                                  BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=168;
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BACSU
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DB 2; Length 80;

Score 8;

0.8%;

Query Match

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EEKDPEEFLN 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=2019606 FubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Anantides F.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Li P.W., Hoskins R.A., Galle R.F., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Am R.H., Doyle C., Baxter E.G., Helt G., Wolson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Brackterin P., Brottier P., Berman B.P., Brokstein P., Borttier P., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Achery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dones M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Borler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.L., Harvey D., Hehman T.J., Hernandez J.R., Houck J., Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Liang Y., Lin X., Liang Y., Lin X., Liang Y., Lin X.,
                                                                                                                                                                                                                                                                                                                                                      Gaps
          Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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ORFNames=CG5603;

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Nooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                          1.3%; Score 12; DB 2; Length 1144;
100.0%; Pred. No. 0.014;
tive 0; Mismatches 0; Indels
                                                                                                           "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                              WormPep; F40F12.5; CE36647.
InterPro; IRR000938; CAP-Gly.
Fam, PP01302; CAP GLY; 1.
Hypothetical Drotein.
SEQUENCE 1144 AA; 128194 MW; 33CCDB2ED3997FE7 CRC64;
                                                                                                                                                                                             Kershaw J.K.;
Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                      EMBL; Z30215; CAF31477.2; -.
WormBase; WBGene00009594; F40F12.5.
                                                            LEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613; Pubmed=9851916;
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Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-Bristol N2;
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                                     NCBI_TaxID=6239;
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                                                                                                        none;
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Liu.X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
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Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
A. Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
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Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., minker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AE003628; AAF52901.1; -.
FlyBase; FBGN0032210; CG5603.
InterPro; IPR00038; CAP-GIY.
Pfam; PF01302; CAP GIIY; 1.
SEQUENCE 517 AA; 58081 MW; AEEE9802F2989404 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Pred. No. 0.88;
0; Mismatches
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MEDLINE=22426065; Pubmed=12537568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22426070; PubMed=12537573;
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nes 10; Conservative
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RESULT 10
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                                           Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Andans M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scheers S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Button G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Abril J.F., Apbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballaw R.M., Basu A., Baxendala J., Baytakatacapil L., Beasley E.M., Beeson K.Y., Bencs P.V., Berman B.P., Bhandari D., Bolchakov S., Botkova D., Botcham D.A., Butler H., Cadleu E., Center A., Chandra I., Cherry J.M., Cawley S., Dallake C., Davenport L.B., Davies P., Chandra I., Cherry J.M., Cawley S., Dallake C., Davenport L.B., Davies P., Butler A., Dangen R.S., Gelbart W.M., Glasser K., Achodon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. Antris N.L., Harvey D., Heiman T.J., Herrandez J.R., Houck J., Houtch J., Adlali M., Kalush F., Karpen G.H., Ke Z., Kunison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kunison J.A., Ketchum K.A., Liu X., Mattei B.E., McIntosh T.C., McLeod M.P., McPherson D., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., Packer D. M., Noy M., Murphy B., Murphy L., Murzhy D.M., Noy M., Murphy B., Murphy L., Muzzhy D.M., Norder J., Shen H., Shen H., Shen H., Shen H., Shen H., Shen E.C., Siden-Kamos I., Simpson M., Stupski M.P., Smith T., Shue B.C., Siden-Kamos I., Simpson M., Stupski M.P., Smith T., Shue B.C., Solen-Kamos I., Simpson M., Stupski M.P., Shu B., Walliams S.M., Woodager, Wollon P.M., Worter E., Wang S., Yon Q.A., Ye J., Walliams S.M., Woodager, Wollon D.R., Woodager, Wollon P.C., Schale M., Shue B.C., Schale M., Woodager, Wollon P., Schale S., Scha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22426065; PubMed=12537568; Carlson J.W., Halpern A., Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Mizny D.M., Nalson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutron G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: Release 3 of the Drosophila
                                     MEDLINE-20196006; PubMed-10731132; DOI=10.1126/science.287.5461.2185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=22426069; PubMed=12537572;
MEDLINE=22426069; PubMed=12537572;
Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              melanogaster euchromatic genome sequence.";
Genome Biol, 3:RESEARCH0079-RESEARCH0079(2002).
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                     Score 12; DB 2; Length 639;
Pred. No. 0.0083;
0; Mismatches 0; Indels
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Celniker S.;
Submitted A.;
Submitted A.;
Submitted A. AL49214.1;
FlyBase; FB900032210; CG5603.
InterProj IPR000318; CAP-Gly.
                                                                                                                                                                                          FlyBase; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                        EMBL, AE003628, AAN10738.1; -.
FlyBase; FBGN0032210; CG5603.
InterPro; IPR000938; CAP-Gly.
Pfam; PF01302; CAP-GLY; 1.
SEQUENCE 639 AA; 72128 MW; 6E29D3B09FP5E55B CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein F40F12.5.
ORFNames=F40F12.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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Best Local Similarity 100.0%; Pred. No. v.v
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                                                                  SEQUENCE FROM N.A.
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Q8SYF0;
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Science 287:2185-2195(2000)
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Q8IPC5;
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ebhydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                         Length 550;
                                                                                                                                                                                                                                                                                                                                                     1.3%; Score 12; DB 2; Length 550
100.0%; Pred. No. 0.0072;
tive 0; Mismatches 0; Indels
                                                   FlyBase;
Submitted (MAR-2004) to the Embary Submitted (MAR-2004) to the Embary Submitted (MAR-2004).

EMBL; AE003628; AANIO3210; CG5603.

InterPro; IPR000938; CAP-Gly.

Pfam; PF01302; CAP_GLY; 1.

Pfam; PF01302; CAP_GLY; 1.

Profits S50 AA; 62083 MW; C87C73651D88FD59 CRC64;
                                                                                                          to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
The 12; Conservative
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SEQUENCE FROM N.A.

MEDLINE=22426065; PubMed=12537568;

MEDLINE=22426065; PubMed=12537568;

MEDLINE=22426065; PubMed=12537568;

MEDLINE=22426065; PubMed=12537568;

MEDLINE=22426065; PubMed=12537568;

Medrorge R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Sarleb J.M., Park S., Pefifer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter (Weinstock G., Scherer S.B., Myers E.W., Gibbs R.A., Rubin G.M.; Milishing a Whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.";

Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Annotation of the Drosophila melanogaster euchromatic genome:
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Eukaryota, Metazoa; Arthropoda, Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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100.0%; Pred. No. 0.0072;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003628; AAN10741.1; -.
MEROPS; C67.001; -.
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Pfam; PF01302; CAP_GLY; 1.
SEQUENCE 551 AA; 62315 WW; 9D4D63B2287B7783 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
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SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           systematic review.";
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Lewis S.E.;
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                                                           357 MELFAVLCIETSHYVAFVKYGKDDSAWLFFDSMADRDGGQNGFNIPQVTPCPEVGEYLKM
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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
                                      852 MELFAVLCIETSHYVAFVKYGKDDSAWLFFDSMADRDGGQNGFNIPQVTPCPEVGEYLKM
  Gaps
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                                                                                                                                                                                                                                                                                                                                                                        Name-agCGS6065; ORFNames=ENSANGG0000016806;
Anopheles gambiae str. PEST.
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anopheles Genome Sequencing Consortium,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
--- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
EMBL, AAABO1008964; EAA12869.1; --
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GO: GO:0004127; F:cysteine-type endopeptidase activity; IEA.
GO: GO:0004221; F:ubiquitin thiolesterase activity; IEA.
GO: GO:0005511; P:ubiquitin-dependent protein catabolism; IEA.
InterPro; IPR001398; CAP-Gly.
InterPro; IPR001394; Peptidase_C19.
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0; Indels
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                                                                                                                                        417 SLEDLHSLDSRRIQGCARRLLCDAYMCMYQSPTMSLYK 454
                                                                                                                  912 SLEDLHSLDSRRIQGCARRLLCDAYMCMYQSPTMSLYK 949
                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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Mismatches
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PROSITE; PS50235; UCH_2_3; 1.
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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18 13; Conservative
Conservative
                                                                                                                                                                                                                                                          PRELIMINARY;
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98;
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SEQUENCE
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Sutton G.G., Regare Y.H., Bland R.G. Champe M. Pefffer B.D.

Bender R.C., Regare Y.H., Bland R.G. Champe M. Pefffer B.D.

Rallew R.W., Bender Y.H., Bland R.G. Champe M. Pefffer B.D.

Abril J. F., Adabyani A., An H.J., Andrews-Fennkoch C., Baldwin D.,

Ballew R.W., Bender B.Y., Berma B.D. Sharkatero P. Ballew R.W.

Ballew R.W., Bender B.Y., Berma B.D. Bhandari D., Bolankov S.,

Bender R.W., Bender B.Y., Berma B.D. Bhandari D., Bolankov S.,

Berkeren D., Bender M.W. Bender B.D. Bhandari D., Bolankov S.,

Borkova D., Benden M.W. Bouck J. Bhandari D., Bolankov S.,

Berkeren D., Bender R.W. Bouck J. Bhandari D., Bolankov S.,

Berkeren D., Borkova D., Bender B. W. Dough S.D. Bhandari D., Bolankov B.C., Danne D.,

Burlin K.J. Svengeliste C., Ferrar C. Ferricas S., Falacinmun M.,

Rolloon D.R. Worngeliste C.C., Ferrar C. Ferricas S., Falacinmun M.,

Rolloon D.R. Worngeliste C.C., Ferrar C. Ferricas S., Falacinmun M.,

Ramin M.J., Malun F., Nathon F., Nathon M. Wallon D.M., New Hortin D. M., Malon D.M., Malon M.W., Malon D.M., Malon M.W., Malon D.M., Malon D.M., Malon M.M., Malo
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Best Local Similarity
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Testis;
PubMed=1247932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moorer T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                                                                                                                                               496 VLAGLELBDECAGCTDGTFRGTRYPTCALKKALFVKLKSCRPDSRFASLQPVSNQ1ERCN
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mutinae; Rattus.
                                                                                                                                                                                                                 Interaction with TRAF2 (by similarity).
Interaction with NEMO (By similarity).
By similarity.
By similarity.
P -> PALS (in isoform 1).
FTIGEVER 011279.
GYPUTGENEPPKIAF -> GYSKNILDQQLKGK (in
                                                                                                                                                                                                       Interaction with TRIP (By similarity) Interaction with TRAF2 (By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          553 SLAFGGYLSEVVEENTPPKMEKEGLEIMIGKKKGIQGHYNSCYLDSTLFCLFAFSS
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952 Missing (in isoform 3).
/FTId=VSP_011280.
403 M -> V (in Ref. 2; BAC30222).
106585 MW; 0ACOC7D4FF215A9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                    Thiol protease;
                                 953 AA
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CAP-Gly 2.
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                        EMBL; AK122389; BAC65671.1; ALT_INIT.
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952 AA;
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Matches 116; Conserv
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                     Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Sucher E.D., Dickson M.C., Krzywinski M.I., Skalska U., Schmutz J., Myers R.W., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marza M.A., Green E.D., Dickson M.C., Grein J.E., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        497 VLAGLELEDECAGCTDGTFRGTRYFTCALKKALFVKLKSCRPDSRFASLOPVSNOIERCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            493 VLAGLELEDECAGCTDGTFRGTRYFTCALKKALFVKLKSCRPDSRFASLQPVSNQIERCN
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S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55, SLAFGGYLSEVVEENTPPKMEKEGLEIMIGKKKGIQCHYNSCYLDSTLFCLFAFSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC062001; AAH82001.1; -.
InterPro; IPR000938; CAP-Gly.
InterPro; IPR001394; Peptidase_C19.
Pfam; PF01302; CAP_GIY; 3.
Pfam; PF01302; CAP_GIY; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106712 MW; 573B59E9BD795252 CRC64;
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ProDom; PD003035; Ribosomal_S3AE; 1.
Ribonucleoprotein; Ribosomal_Drotein.
SEQUENCE 454 AA; 52009 WW; 8828B384B9F8F69F CRC64;
                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Director MGC Project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. SEQUENCE 953 AA; 1
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             EVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK 530
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080TQ2; Q80VB3; Q8BXZ3; Q8BXL9; Q8CGB0;
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Probable ubiquitin carboxyl-terminal hydrolase CYLD (EC 3.1.2.15)
Probable ubiquitinating enzyme.CYLD).
(Ubiquitininating enzyme.CYLD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISOFORM 1).
STRAIN=C57BL/6J; TISSUE=Cerebellum, and Hypothalamus;
STRAIN=C354683; PubMed=12466851; DOI=10.1038/nature01266;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Okazaki Y., Furuno M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
                                                                                                                                                       YGYVCATKIMKLRKILEKVEAASGPTSEEKDPEEFINILFHHILRVEPLLKIRSAGQKVQ
                                                                                                                                                                                          DCYFYQIFMEKNEKVGVPT1QQLLEWSFINSNLKFAEAPSCL11QMPRFGKDFKLFKKIF
                                                                                                                                                                                                                                                                                                                                               MADRDGGQNGFNI PQVTPCPEVGEYLKMSLEDLHSLDSRR I QGCARRLLCDAYMCMYQSP
                                                                                                                                                                                                                                                                                                                                                            YGYVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRVEPLLKIRSAGQKVQ
                                                                                                                                                                                                          DCYFYQIFMEKNEKVGVPTIQQLLEWSFINSNLKFABAPSCLIIQMPRFGKDFKLFKKIF
                                                                                                                                                                                                                                                                                             LINHKYNPVSLPKDLPDWDWRHGCI PCQNMELFAVLCI ETSHYVAFVKYGKDDSAWLFFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S., Nakajima D., Nagase T., Ohara O., Koga H.; "Prediction of the coding sequences of mouse homologues of KIAA gene: II. The complete nucleotide sequences of 400 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries.";
                                                    ALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK
                                                                                        KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVBYYSETQELLRTEIVNPLRI
                                                                                                                                                                                                                                            PSLELNITDLLEDTPROCRICGGLAMYECRECYDDPDISAGKIKOFCKTCNTQVHLHPKR
                                                                                                                                                                                                                                                                                                                    LNHKYNPVSLPKDLPDWDWRHGCIPCQNMELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
                                      ALFVKLKSCRPDSRFASLQPVSNQI ERCNSLAFGGYLSEVVEENTPPKMEKEGLE1M1GK
                                                                                                      KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRI
                                                                                                                                                                                                                                                                    PSLELNITDLLEDTPROCRICGGLAMYECRECYDDPDISAGKIKOFCKTCNTQVHLHPKR
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 3), AND SEQUENCE OF 1-620 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Cyld; Synonyms=Cyld1, Kiaa0849;
Mus musculus (Mouse).
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MEDLINE=22579291; PubMed=12693553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 10:35-48(2003).
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Konni A., Kawaji H., Kawasawa H., Kedzierski R.M., King B.L.,

Konni A., Kawaji H., Kawasawa H., Kedzierski R.M., King B.L.,

Romagaya A., Kurcockhi I.V., Merchicumi L., McKenzie L., Mikih.

Ray Maglott D. E., Maltasa L., Marchicumi L., Kedzierski R.M., King B.L.,

Maglott D. E., Maltasa L., Marchicumi L., Kedzier L., Mikih.

Ray Maglott D. E., Maltasa L., Marchicumi L., Kedzie L., Mikih.

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Ray Ray M., Manday B. C., Read D.J., Bank J., Ming B.Z., Ringeald M.,

Sandelin A., Schmeider C., Semple C.A., Strange B.C., Tomica M.,

Nerrado R., Wagner L., Wahlsta M., Strawa K., Ashawa T., Wanda E.,

Ray Warada, M., Walawa W., Maltang M., Manday J., Manda P., Wala B.,

Rayazada, M., Sakai K., Samahi D., Bahbeta K., Shinada W., Kagwa I.,

Rayazada, M., Sakai K., Samahi D., Bahbeta K., Shinada W., Kagwa I.,

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Rayazada, M., Sakai K., Samahi D., Macrescon R., Lander E.S., Rogers J.,

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Rayazada, M., Sakai K., Samahi D., Samahi D., Shinada W., Shinada W., Shinada W.,

Rayazada, M., Sakai K., Samahi D., Samahi B., Maltanga W., Shinada ```

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Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
 SEQUENCE OF 397-956 FROM N.A.

TISSUE-Umbilical cord blood;

MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;

Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;

"Cloning and functional analysis of cDNAs with open reading frames for stem/progenitor cells.";

genome Res. 10:1546-1560(2000).
 TISSUE SPECIFICITY: Detected in fetal brain, testis, and skeletal TISSUE SPECIFICITY: Detected in fetal brain, testis, and skeletal muscle, and at a lower level in adult brain, leukocytes, liver, heart, kidney, spleen, ovary and lung. Isoform 2 is found in all tissues except kidney.

DISEASE: Defects in CYLD are the cause of familial cylindromatosis
 "CYLD is a deubiquitinating enzyme that negatively regulates NF-kappaB activation by TNFR family members.";
 Kovalenko A., Chable-Bessia C., Cantarella G., Israeel A., Wallach D.,
 INTERACTIONS WITH NEMO AND TRAF2, AND MUTAGENESIS OF SER-457
 tumour suppressor CYLD negatively regulates NF-kappaB signalling
 ģ
 EXP. Wed. 198:1959-1964(2003).

EXP. Wed. 198:1959-1964(2003).

EXP. Med. 198:1959-1964(2003).

Pathway. Has deubiquitinating activity that is directed towards non-Lys-48-linked polyubiquitin chains. The inhibition of NF-kappa-B activation is mediated at least in part, by the deubiquitination and inactivation of TRAF2 and, to a lesser extent, TRAF6.

CATALITIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
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 Brunmelkamp T.R., Nijman S.M.B., Dirac A.M.G., Bernards R.; Loss of the cylindromatosis tumour suppressor inhibits apoptosis activating NF-kappab ... Nature 424:797-801(2003).
 PubMed=14676304; DOI=10.1084/jem.20031187;
Regamey A., Hohl D., Liu J.W., Roger T., Kogerman P., Toftgaard
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.
 "The tumor suppressor CYLD interacts with TRIP and regulates negatively nuclear factor kappaB activation by tumor necrosis
 FUNCTION, INTERACTION WITH NEMO, AND MUTAGENESIS OF CYS-601 bubMed=12917689; DOI=10.1038/nature01803; Trompouki E., Hatzivassiliou E., Tsichritzis T., Farmer H., Ashworth A., Mosialos G.;
 FUNCTION, INTERACTION WITH NEMO, AND MUTAGENESIS OF CYS-601
 FUNCTION, SUBCELLULAR LOCATION, AND INTERACTION WITH TRIP
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 Event=Alternative splicing; Named isoforms=2;
 SUBGNIT: Interacts with NEWO, TRAF2 and TRIP. SUBCELLULAR LOCATION: Perinuclear region. ALTERNATIVE PRODUCTS:
 PubMed=12917690; DOI=10.1038/nature01811;
 IsoId=Q9NQC7-1; Sequence=Displayed;
 PubMed=12917691; DOI=10.1038/nature01802;
 Nature 424:801-805(2003).
 Nature 424:793-796(2003).
 ubiquitin + a thiol.
 deubiquitination.
 Courtois G.;
 AND HIS-871.
 Name=1
 FUNCTION.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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 403
 463
 351 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPVNSL 410
 411 TTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL 470
 464 EVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK 523
(CYLD) [MIM:132700]; also known as turban tumor syndrome or dermal
 344 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL
 404 ITENRFHSLPFSLIKMPNINGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 601 C->S: Loss of deubiquitinating activity.
871 H->N: Loss of deubiquitinating activity.
107315 MW; 01831F9A83424631 CRC64;
 Gaps
 0;
 GO; GO:0004221; F:ubiquitin thiolesterase activity; NAS. GO; GO:0006511; P:ubiquitin-dependent protein catabolism; NAS. InterPro; IPR000938; CAP-G1y. InterPro; IPR001394; Peptidase_C19.
 By similarity.
By similarity.
By similarity.
(In isoform 2).
/FIIG-VSP 011277.
S->A: Abolishes binding to TRAF2.
 DB 1; Length 956;
 0; Indels
 Pfam; PF01302; CAP GLY; 3.

PROSITE; PS00845; CAP GLY 1; FALSE NEG.

PROSITE; PS00945; CAP GLY 2; 2.

PROSITE; PS00973; UCH 2 1; PALSE NEG.

PROSITE; PS00973; UCH 2 2; PALSE NEG.

PROSITE; PS50235; UCH 2 2; 1.

Alternative splicing; Anti-oncogene; Hydrolase; Repeat;
 conjugation pathway.
198
CAP-Gly 1.
535
CAP-Gly 2.
10 Interaction with TRIP.
169
Interaction with TRAF2.
184
Interaction with NEMO.
 Score 606; DF
 100.0%; Pred ...
 AB020656; BAA74872.2; ALT INIT.
 GO; GO:0005856; C:cytoskeleton; NAS
 EMBL; AJ250014; CAB93533.1; -
 63.9%;
 606, Conservative
 Genew; HGNC:2584; CYLD.
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 956 AA;
 Similarity
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April 18, 2005, 09:15:43; Search time 65 Seconds (without alignments) 7476.356 Million cell updates/sec

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949
1 MSSGLWSQEKVTSPYWEERI.....RLLCDAYMCMYQSPTMSLYK 949 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters: . 0 Word size :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|           | Description    | Q9nqc7 homo sapien | mus m      | Q66h62 rattus norv |        |        | 4 drosophila |        |        |        |        | =      |        | Q8ex39 mycoplasma | ~          |                          |        |        |        |        |        |        | Q621g0 burkholderi | Q63wb0 burkholderi | Q9ezu8 serratia ma | Q8n4a4 homo sapien | Q6a178 cryptospori | Q9awt2 oryza sativ | Q6mjh4 bdellovibri | Q9vhv0 drosophila | 001754 caenorhabdi | Q928r6 listeria in |
|-----------|----------------|--------------------|------------|--------------------|--------|--------|--------------|--------|--------|--------|--------|--------|--------|-------------------|------------|--------------------------|--------|--------|--------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|
| SUMMAKIES | ΙΩ             | CYLD HUMAN         | CYLD MOUSE | <u> Q66н6</u> 2    | Q6TXJ6 | 070414 | Q8IPC4       | QBIPC3 | QBIPCS | Q8SYF0 | Q7JMS4 | Q9VL04 | Q6AQ83 | Q8EX39            | YYBA BACSU | 07 <u>0</u> Y <u>1</u> 6 | Q9HX43 | Q9GKF5 | Q7SFV2 | Q9U0S3 | Q8VXG1 | Q7PJA3 | Q62LG0             | Q63WB0             | Q9EZU8             | Q8N4A4             | Q6A178             | Q9AWT2             | обмлн4             | O3HA60            | 001754             | G6PI_LISIN         |
|           | DB             | -                  | н          | ~                  | ~      | ~      | ~            | ~      | 7      | ~      | 7      | ~      | 7      | 7                 | -          | 7                        | ~      | ~      | ~      | ~      | ~      | ~      | ~                  | 7                  | ~                  | 7                  | ~                  | ~                  | ~                  | 7                 | 7                  | н                  |
|           | Length         | 926                | 952        | 953                | 454    | 778    | 220          | 551    | 639    | 939    | 1144   | 517    | 225    | 80                | 150        | 212                      | 215    | 216    | 225    | 236    | 237    | 258    | 274                | 276                | 353                | 354                | 366                | 371                | 401                | 418               | 423                | 450                |
| æ         | Query<br>Match | 63.9               | 12.2       | 12.2               | 10.3   | 1.4    | 1.3          | 1.3    | 1.3    | 1.3    | 1.3    | 1.1    | •      | ٠                 | 0.8        | ٠                        | 0.8    | 0.8    | ٠      |        | 0.8    | •      | •                  | ٠                  | •                  | •                  | ٠                  | ٠                  | 0.8                | •                 | •                  | •                  |
|           | Score          | 909                | 116        | 116                | 98     | 13     | 12           | 12     | 12     | 12     | 12     | 10     | σ      | <b>6</b> 0        | 80         | 80                       | œ      | 60     | æ      | 89     | œ      | œ      | ω                  | ω                  | 80                 | 80                 | 89                 | 80                 | 80                 | 8                 | 80                 | 80                 |
|           | Result<br>No.  | 1                  | 7          | М                  | 4      | Ŋ      | 9            | 7      | 89     | σ      | 10     | 11     | 12     | 13                | 14         | 15                       | 16     | 17     | 18     | 19     | 20     | 21     | 22                 | 23                 | 24                 | 25                 | 56                 | 27                 | 28                 | 53                | 30                 | 31                 |

| Q894r7 listeria mo Q71x61 listeria mo Q71x61 listeria mo O446r7 caenorhabdi Q6nac1 rhodopseudo Q00557 mesocricetu P5310 saccharomyc Q818V0 drosophila Q8y2q7 ralstonia s Q8k2q7 ralstonia s Q8t2q7 seudomonas Q912b2 pseudomonas Q912b2 pseudomonas Q912b2 leptospira Q9rxg0 deinococcus Q72sg2 leptospira |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| G6PI_LISMO<br>041617<br>041617<br>041617<br>06NAC1<br>CP11_MEGAU<br>AG12_YEAST<br>Q818VO<br>ACEK_RALSO<br>Q8K7W4<br>Q912B2<br>028905<br>028905<br>028905<br>028905<br>028905<br>028905<br>028905<br>028905<br>028905                                                                                       |
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| 450<br>450<br>458<br>522<br>524<br>524<br>524<br>555<br>608<br>625<br>625<br>627<br>753<br>760                                                                                                                                                                                                             |
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| <b>&amp; &amp; </b>                                                                                                                                                                                  |
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## ALIGNMENTS

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The invention relates to novel genes (ABL89449-ABL90853) and proteins

(ABB89040-ABB90444) useful for preventing, treating or ameliorating

medical conditions e.g. by protein or gene therapy. The genes are

isolated from a range of human tissues disclosed in the specification.

The nucleic acids, proteins, antibodies and (ant) agonists are useful in

the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and

covarian cancer and other cancers of the adrenal gland, bone, bone marrow,

breast, gastrointestinal tract, lung, or urogenital; (b) immune

disorders e.g. Addison's disease, allergies, autoimmune haemolytic

anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,

multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)

cardiovascular disorders such as mycoardial ischaemias; (d) wound healing

cardiovascular diseases e.g. cerebral anoxia and epilepsy; and (f)

infections. Note: The sequence data for this patent did not form part of

the printed specification, but was obtained in electronic format directly

crome with the printed specification, but was obtained in electronic format directly

contains the printed specification of the printed pri
 Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
 EVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK 504
EVGSLAEVKENPPFYGVIRWIGOPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK
 Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders.
 Claim 11; SEQ ID NO 1609; 2081pp + Sequence Listing; English
 21.9%; Score 208; DB 5; Length 261; 100.0%; Pred. No. 1.7e-197; ive 0; Mismatches 0; Indels
 ABB89233 standard; protein; 261 AA
 Human polypeptide SEQ ID NO 1609.
 18-MAY-2001; 2001WO-US016450.
 19-MAY-2000; 2000US-0205515P.
 (HUMA-) HUMAN GENOME SCI INC
 (first entry)
 Query Match
Best Local Similarity
Matches 208; Conserva
 Birse CE, Rosen CA;
 WPI; 2002-122018/16.
N-PSDB; ABL89642.
 Sequence 261 AA;
 WO200190304-A2.
 Homo sapiens.
 24-MAY-2002
 29-NOV-2001.
 ABB89233;
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XX ABB89233
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27-SEP-2000;
29-SEP-2000;
 17-NOV-2000;
 08-NOV-2000;
 14-SEP-2000;
 14-SEP-2000;
 21-SEP-2000;
 29-SEP-2000;
 29-SEP-2000;
 02-OCT-2000;
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The present invention relates to the isolation of novel human enzyme polypeptides, and the CDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the disorders including hyperproliferative disorders (e.g. cancer), meurological disorders (e.g. AIDS) autoimmune disorders (e.g. anthal).

Immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. asthma), cardiovascular disorders (e.g. AIDS) inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. altherosclerosis), blood-related disorders (e.g. inflammatory disorders (e.g. infertility) and infertility and also be used in gene therapy. AAU22915-AAU23814 represent the novel human enzyme polypeptides of the invention can also be used in gene therapy. AAU22915-AAU23814 represent the novel human enzyme polypeptides of the invention of a lectronic format directly from WIPO at the print format directly from WIPO at the print sequences.
 344 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL 403
 TTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL 463
 TIENRFHSLPFSLIKMPNINGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL 444
 Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
 0; Gaps
 23.9%; Score 227; DB 4; Length 558; 100.0%; Pred. No. 4.2e-216; ive 0; Mismatches 0; Indels
 Claim 11; SEQ ID NO 1207; 1180pp; English
 Rosen CA, Barash SC, Ruben SM;
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-024924F.
17-NOV-2000; 2000US-024924F.
17-NOV-2000; 2000US-024926F.
17-NOV-2000; 2000US-025191P.
01-DEC-2000; 2000US-025191P.
05-DEC-2000; 2000US-025196F.
06-DEC-2000; 2000US-025186F.
08-DEC-2000; 2000US-025186F.
08-DEC-2000; 2000US-025186F.
08-DEC-2000; 2000US-025186F.
08-DEC-2000; 2000US-025186F.
 (HUMA-) HUMAN GENOME SCI INC
 Matches 227; Conservative
 Local Similarity
 WPI; 2001-465566/50
 N-PSDB; AAS41081
 Sequence 558 AA;
 325
 404
 385
 Query Match
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us-09-671-687a-3.0ligo.rag

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306 ALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVVBENTPPKMEKEGLEIMIGK 365
 YGYVCATKIMKLRKILEKVEAASGFTSEEK 673
 Novel human enzyme polypeptide #297.
 Ą
 AAU23211 standard; protein; 558
 2000US-0214886P.
 2000US-0217487P.
 2000US-0220963P.
2000US-0220964P.
2000US-0224518P.
 2000US-0225213P.
2000US-0225214P.
2000US-0225266P.
 2000US-0225267P.
2000US-0225268P.
 17-JAN-2001; 2001WO-US001239
 2000US-0209467P
 2000US-0216647P
 2000US-0216880P
 2000US-0218290P
 2000US-0189874P
 2000US-0225270P
 2000US-0225447P
 2000US-0229287P
 (first entry)
 WO200155301-A2
 26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
 14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
 Homo sapiens
 16-MAR-2000;
17-MAR-2000;
 18-DEC-2001
 18-APR-2000;
 02-MAR-2000;
 14-AUG-2000;
 14-AUG-2000;
 14-AUG-2000;
 02-AUG-2001
 584
 AAU23211;
 644
 RESULT 14
 AAU2321
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 The present invention describes primer sets for synthesising 5602 full-

[1 length cDNAs defined in the specification. Where a primer set comprises:
[2 [4] an Oligo-dr primer and an Oligonucleotide comprises one of the 5602
[2 complementary strand of a polynucleotide which comprises one of the 5602
[2 complementary strand of a polynucleotides; or (b) a combination
[2 complementary strand of a polynucleotide which comprises a 5'-end
[2 complementary strand of a polynucleotide which comprises a 5'-end
[2 sequence and an Oligonucleotide comprises a 3'-end sequence complementary to a
[2 complementary strand of a polynucleotide which comprises a 1'-end sequence complementary to a
[2 complementary strand of a polynucleotide which comprises a 1'-end sequence
[3 complementary strand of a polynucleotide sequence
[4 complementary strand of a polynucleotide of the 5'-end sequence
[5 complementary strand of a polynucleotides and the complementary to a
[5 complementary strand of a polynucleotide of the 5'-end sequence
[5 complementary strand of a polynucleotide of the 5'-end sequence
[6 complementary strand of a polynucleotide of the 5'-end sequence
[7 complementary strand of a polynucleotides
[8 comprises at least 15 nucleotides and the compination of the full-length cDNAs. The primers are useful for synthesising polynucleotides,
[8 complementary strand of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs represent human amino acid sequences; and AAH13632 to AAH13632 represent coligonucleotides, all of which are used in the exemplification of the present invention
 185
 583
 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
 344 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL 403
 BVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK 305
 TENREHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 ALFVKLKSCRPDSRFASLQPVSNQIBRCNSLAFGGYLSEVVBENTPPKMEKEGLEIMIGK
 TTENRFHSLPPSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 EVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK
 Gaps
 Human; primer; detection; diagnosis; antisense therapy; gene therapy
 Yamamoto J;
 ;
0
 Claim 8; SEQ ID NO 18587; 2537pp + Sequence Listing; English.
 34.8%; Score 330; DB 4; Length 476; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels
 Saito K, Ya
, Otsuki T;
 nikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
 Isogai T, Nishikawa T,
 27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-0018376.
09-JUN-2000; 2000JP-00241899.
 28-JUL-2000; 2000EP-00116126
 Best Local Similarity 100.
Matches 330; Conservative
 Sugiyama T,
 (HELI-) HELIX RES INST.
 WPI; 2001-318749/34.
 Sequence 476 AA;
 Homo sapiens
 EP1074617-A2
 29-JUL-1999;
 07-FEB-2001
 Ishii S,
 126
 404
 186
 464
 246
 Query Match
 524
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425
 Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic; nephrotropic; anticoagulant.
 366 KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRI
KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRI
 426 YGYVCATKIMKLRKILEKVEAASGFTSEEK 455
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 The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with noctropic, immunosuppressent and cytostatic activity. The polynucleotides are useful immunosuppressent and cytostatic activity. The polynucleotides are useful on gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous fijuries, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, changer Syndrome. Other uses include the Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assaays for receptor activity, arthritis and inflammation, leuksemias and sassays for receptor activity, arthritis and inflammation, leuksemias and C.N.S disorders. Note: The sequence data for this patent did not form
 500
 ě,
 nucleic acids and polypeptides, useful for treating disorders such
 Zhao
 KDDSAMLFFDSMADRDGGQNGFNI PQVTPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLL
 EKEGLEIMIGKKKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQEL
 LRTEI VNPLRIYGYVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRVEPL
 381 LRTEIVNPLRIYGYVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRVEPL
 GKDFKLFKKIFPSLELNITDLLEDTPRQCRICGGLAMYECRECYDDPDISAGKIKQFCKT
 LKIRSAGQKVQDCYFYQIFMEKNEKVGVPTIQQLLEWSFINSNLKFAEAPSCLIIQMPRF
 LKIRSAGQKVQDCYFYQIFMEKNEKVGVPTIQQLLEWSFINSNLKFAEAPSCLIIQMPRF
 CNTQVHLHPKRLNHKYNPVSLPKDLPDWDWRHGC1PCQNMELFAVLC1ETSHYVAFVKYG
 KDDSAWLFFDSMADRDGGQNGFNI PQVTPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLL
 EKEGLEIMIGKKKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQEL
 GKDFKLFKKIFPSLELNITDLLEDTPROCRICGGLAMYECRECYDDPDISAGKIKQFCKT
 Wang
 ٦,
 ö
 Ren F,
Zhang
 Length 698;
 Indels
 Qian XB,
Yang Y,
 ..
0
 DB 4;
 Ma Y,
Xue AJ,
 English.
 Score 363; DB; Pred. No. 0; 0; Mismatches
 NO:18587
 Chen R,
 rman T, Xu C,
Drmanac RT;
 SEQ ID NO 5971; 10078pp;
 Š
 as central nervous system injuries.
 part of the printed specification
 38.00
100.08; Pr
 standard; protein; 476
 Human protein sequence SEQ ID
 Asundi V, (
Wehrman T,
 38.3%;
 Conservative
 Wang Z, Weh
Goodrich R,
 2001-442253/47.
 Similarity
Liu C,
 935
 683
 WPI; 2001-442253,
N-PSDB; AAI60196
 Sequence 698 AA;
 _6
_6
 CDA
 26-JUN-2001
 363;
 441
 621
 633
 573
 321
 693
 501
 873
 681
 AAB95719
 AAB95719;
 753
 813
 Query Match
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Matches
 Novel
 Tang
Wang
Zhou
 RESULT 13
 AAB9571
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 703
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 823
 883
 890
 950
 DCYFYQIFMEKNEKVGVPTIQQLLEWSFINSNLKFAEAPSCLIIQMPRFGKDFKLFKKIF 763
 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; palipheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral scleroals; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
 YGYVCATKIMKLKKILEKVEAASGFTSEEKDPEBFLNILFHHILRVEPLLKIRSAGQKVQ
 ALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKWEKEGLEIMIGK
 KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEI VNPLRI
 YGYVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRVEPLLKIRSAGQKVQ
 DCYFYQI FMEKNEKVGVPTIQQLLEMSFINSNLKFAEAPSCLIIQMPRFGKDFKLFKKI F
 PSLELNI TDLLEDTPRQCRI CGGLAMYECRECYDDPDI SAGKI KQFCKTCNTQVHLHPKR
 LNHKYNPVSLPKDLPDWDWRHGCI PCQNMELFAVLCI ETSHYVAFVKYGKDDSAWLFFDS
 LNHKYNPVSLPKDLPDWDWRHGCIPCQNMELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
 MADRDGGONGFNI PQVTPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLLCDAYMCMYQSP
 MADROGGONGFNI PQVT PCPEVGEYLKWSLEDLHSLDSRR I QGCARRLLCDAYMCMYQSP
 KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRI
 PSLELNITDLLEDTPROCRICGGLAMYECRECYDDPDISAGKIKOFCKTCNTOVHLHPKR
 Ā
 polypeptide SEQ ID NO 5971
 AAM41040 standard; protein; 698
 99US-00471275.
2000US-00488725.
2000US-00552317.
2000US-00598042.
2000US-00620312.
 2000US-00653450.
2000US-00662191.
2000US-00693036.
 26-DEC-2000; 2000WO-US034263
 2000US-00727344
 (first entry)
 TMSLYK 949
 926
 (HYSE-) HYSEQ INC
 TMSLYK
 WO200153312-A1
 25-APR-2000;
20-JUN-2000;
19-JUL-2000;
 03-AUG-2000;
 Ното варіеля
 23-DEC-1999;
21-JAN-2000;
 19-OCT-2000;
 22-OCT-2001
 26-JUL-2001
 leukaemia
 AAM41040;
 591
 644
 764
 324
 884
 944
 951
 584
 651
 704
 171
 331
 891
 471
 Human
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RESULT 12 AAM41040

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ADQ95920 standard; protein;
 Matches
 RESULT 11
ADQ95920
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 527
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 463
 467
 523
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 587
 643
 647
 703
 763
 767
 823
 827
 943
 707
 887
 947
 The invention relates to purified proteins and genes encoding them, that are involved in T cell activation (I) and has an amino acid deletion, substitution or addition in the amino acid sequences. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of autoimmune disease (rheumatoid arthritis, asthma, multiple sclerosis and diabetes), allergic disease, infectious disease, AIDS, and acute or chronic rejection at organ transplant or bone marrow transplant. This sequence corresponds to a protein involved in T cell activation.
 d protein involved in T cell activation, useful for preventing and/or treating acquired immunodeficiency utoimmune (e.g. rheumatoid arthritis, and diabetes), allergic
 ALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK
 YGYVCATKIMKLKKILEKVBAASGFTSEBKDPEBFLNILFHHILRVBPLLKIRSAGGKVQ
 MADRDGGQNGFNI PQVTPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLLCDAYMCMYQSP
 344 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL
 TTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 TTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 EVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK
 ALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK
 KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRI
 KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRI
 YGYVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRVEPLLKIRSAGOKVQ
 DCYFYQIFMEKNEKVGVPTIQQLLEWSFINSNLKFAEAPSCLIIQMPRFGKDFKLFKKIF
 DCYFYQIFMEKNEKVGVPTIQQLLEWSFINSNLKFAEAPSCLIIQMPRFGKDFKLFKKIF
 PSLELNITDLLEDTPRQCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHPKR
 PSLELNITDLLEDTPROCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHPKR
 LNHKYNPVSLPKDLPDWDWRHGCIPCQNMELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
 LNHKYNPVSLPKDLPDWDWRHGCIPCQNWBLFAVLCIETSHYVAFVKYGKDDSAWLFFDS
 MADRDGGQNGFNI PQVTPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLLCDAYMCMYQSP
 Gaps
 ;
 Length 953;
 1; Indels
 ..
8
 Score 505; DB
Pred. No. 0;
0; Mismatches
 DB
 Claim 1; SEQ ID NO 94; 2828pp; English
ASAHI KASEI PHARMA CORP
 53.2%;
 al Similarity 99.8
605; Conservative
 infectious diseases.
 ŝ
 autoimmune
 2004-593134/57
 Yoneta
 TMSLYK 949
 TMSLYK 953
 N-PSDB; ADQ95915
 Sequence 953 AA;
 purified
 diagnosing,
 À
 348
 404
 408
 464
 468
 524
 528
 584
 588
 648
 708
 768
 824
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 Query Match
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The invention relates to purified proteins and genes encoding them, that are involved in T cell activation (I) and has an amino acid deletion, substitution or addition in the amino acid sequences. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of autoimmune disease (rheumatoid arthritis, asthma, multiple sclerosis and diabetee), allergic disease, infectious disease, ALDS, and acute or chronic rejection at organ transplant or bone marrow transplant. This sequence corresponds to a protein involved in T
 EVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK 523
 New purified protein involved in T cell activation, useful for diagnosing, preventing and/or treating acquired immunodeficiency syndrome, autoimmune (e.g. rheumatoid arthritis, and diabetes), allergic
 RSELFYTLINGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL
 TTENREHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVOESPPLAMPPGUSHGL
 antiallergic; antiarthritic; antiasthmatic; antidiabetic; anti-HIV; antimicrobial; antirheumatic; immunosuppressive; neuroprotective; gene therapy; T cell activation; diagnosis; autoimmune disease; rheumatoid arthritis; asthma; multiple sclerosis; diabetes; allergic disease; infectious disease; AIDS; chronic rejection; organ; bone-marrow transplant.
 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL
 TTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMBELNTAPVQESPPLAMPPGNSHGL
 Gaps
 .
 8; Length 956;
 Indels
 ;
 В
 Mismatches
 .
 cell activation associated protein #49.
 53.2%; Score 505; 99.8%; Pred. No. 0;
 Claim 1; SEQ ID NO 98; 2828pp; English
 (ASAH-) ASAHI KASEI PHARMA CORP
 í
O
 26-DEC-2002; 2002JP-00376365.
27-DEC-2002; 2002US-0436473P.
25-APR-2003; 2003US-00122113.
28-APR-2003; 2003US-0465792P.
 25-DEC-2003; 2003WO-JP016715
 22-OCT-2003; 2003US-0512846P.
 21-OCT-2003; 2003JP-00360559
 605; Conservative
 and infectious diseases
 2004-593134/57.
 (first
 Matsuda A, Yoneta
 Similarity
 N-PSDB; ADQ95919
 WO2004058805-A2
 Sequence 956 AA;
 07-OCT-2004
 15-JUL-2004
ADQ95920;
 344
 351
 464
 404
 411
 Query Match
 Local
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410 463

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TTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 Homo sapiens.
 07-OCT-2004
 15-JUL-2004.
 186
 366
 486
 ADQ95916;
 464
 246
 524
 306
 584
 704
 764
 824
 884
 944
404
 RESULT 10
 ADQ9591
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 The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification, where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprisementary to the
complementary strand of a polyuncleotide comprises one of the 5602
nucleotide sequences defined in the specification, where the
complementary strand of a polyuncleotide which comprises one of the 5602
complementary strand of a polyuncleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide comprises at least 15 nucleotides and the combination of
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence, where the
coligonucleotide comprises at least 15 nucleotides and the combination of
complementary strand of a polynucleotide so the 5'-end sequence of a polynucleotide of
complementary strand of a polynucleotide size and the combination of
complementary strand of a polynucleotide size and sequence where the
coligonucleotide which comprises at least 15 nucleotides and the combination of
colification. The primer sets can be useful for synthesising polynucleotides,
conficularly full-length cDNAs. The primers are also useful for the
chetction and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
AAH13633 to AAH18742 repersent human cDNA sequences; AAB92446 to AAB95893
represent human amino acid sequences; and ANH3629 to AAH13632 represent
complementary strand of the rempile of the
coligonucleotides, all of which are used in the exemplification of the
 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
 detection; diagnosis; antisense therapy; gene therapy.
 Yamamoto J;
 Claim 8; SEQ ID NO 18843; 2537pp + Sequence Listing; English.
 Score 505; DB 4; Length 731; Pred. No. 0;
 Isogai T, Nishikawa T, Hayashi K, Saito K, Y.
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 Human protein sequence SEQ ID NO:18843
 AAB95828 standard; protein; 731 AA
 29-JUL-1999; 99JP-00248036.
27-ANG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
 Query Match
Best Local Similarity 99.8%;
Matches 605; Conservative 0
 28-JUL-2000; 2000EP-00116126
 (first entry)
 (HELI-) HELIX RES INST.
 WPI; 2001-318749/34.
 Sequence 731 AA;
 Human; primer;
 Homo sapiens
 EP1074617-A2.
 26-JUN-2001
 Ota T, Is
Ishii S,
 AAB95828;
RESULT 9
 AAB9582
```

344 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL 403 

8

Gaps

; 0

1; Indels

0; Mismatches

```
643
 425
 545
 823
 EVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK
 ALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK
 KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLGPKEKNDVBYYSETQELLRTEIVNPLRI
 DCYFYQIFMEKNEKVGVPT1QQLLEWSFINSNLKFAEAFSCL11QMPRFGKDFKLFKKIF
 DCYFYQI FMEKNEKVGVPT1QQLLEWSFINSNLKFAEAPSCL11QMPRFGKDFKLFKKI F
 546 PSLELNITDLLEDTPRQCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHPKR
 TTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 EVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK
 ALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK
 KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRI
 PSLELNITOLLEDTPROCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHPKR
 LNHKYNPVSLPKDLPDWDWRHGCIPCQNWELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
 MADRDGGQNGFNIPQVTPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLLCDAYMCMYQSP
 antimicrobial; antirheumatic; immunosuppressive; neuroprotective; gene therapy; T cell activation; diagnosis; autoimmune disease; rheumatoid arthritis; asthma; multiple solerosis; diabetes; allergic disease; infectious disease; AIDS; chronic rejection; organ;
 antiallergic; antiarthritic; antiasthmatic; antidiabetic; anti-HIV;
 cell activation associated protein #47.
 ADQ95916 standard; protein; 953 AA
 27-DEC-2002; 2002US-0436473P.
25-APR-2003; 2003JP-00121113.
28-APR-2003; 2003US-0465792P.
21-OCT-2003; 2003US-0512846P.
 25-DEC-2003; 2003WO-JP016715
 2002JP-00376365
 (first entry)
 bone-marrow transplant
 TMSLYK 949
 726 TMSLYK 731
 WO2004058805-A2.
 26-DEC-2002;
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770
 950
523
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 643
 650
 703
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 830
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 890
 943
 Diagnosing breast cancer comprises comparing the level of expression of genes or gene products in a first biological sample taken from a patient with that in a normal patient sample.
 DCYFYQIFMEKNEKVGVPT1QQLLEMSFINSNLKFAEAPSCLIIQMPRFGKDFKLFKKIF
 MADROGGONGFNIPOVTPCPEVGEYLKWSLEDLHSLDSRRIQGCARRLLCDAYMCMYOSP
 EVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK
 LINHKYNPVSLPKDLPDWDWRHGCIPCQNWELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
 ALFVKLKSCRPDSRPASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK
 KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVBYYSETQELLRTEIVNPLRI
 KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRI
 YGYVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRVEPLLKIRSAGOKVO
 DCYFYQIFMEKNEKVGVPT1QQLLEWSFINSNLKFAEAPSCLIIQMPRFGKDFKLFKKIF
 PSLELNITDLLEDTPRQCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHPKR
 LNHKYNPVSLPKDLPDWDWRHGCIPCQNMELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
 MADRDGGQNGFNIPQVTPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLLCDAYMCMYQSP
 Cytostatic; breast cancer; cancer; human; DKFZp586D1122.
 ADR99244 standard; protein; 960 AA
 27-FEB-2004; 2004WO-US007268
 28-FEB-2003; 2003US-0450655P
 (first entry)
 (FARB) BAYER PHARM CORP.
 SEQ ID
 Bigwood
 WPI; 2004-653556/63.
N-PSDB; ADR99117.
 TMSLYK 949
 TMSLYK 956
 WO2004078035-A2.
 DKFZp586D1122,
 Homo sapiens
 02-DEC-2004
 Eveleigh D,
 16-SEP-2004
 531
 ADR99244;
 471
 524
 584
 591
 651
 824
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The present in a patient. The method comparison comparing the level of expression of one or more genes or gene products in a biological sample from the patient with that in a normal patient sample, where a difference in the gene expression in the first sample compared to that in the second sample is a diagnostic of the disease. Also claimed are: method (M2) for distinguishing between normal and disease tissues; method (M3) for distinguishing between normal and disease tissues; method (M3) for monitoring the response of a breast cancer patient to treatment with an anti-cancer agent; method (M4) for identifying a compound for treating comprising two or more probes corresponding to genes selected from ADR99122-ADR991248. In M1 and M2 the genes are selected from ADR99122-ADR991248. In M1 and M2 the genes are selected from ADR99124 and the gene products are polypeptides selected from ADR99124 and the gene products are polypeptides selected from ADR99124 and the gene products are polypeptides selected from ADR99124 and the gene products are polypeptides selected from ADR99124 and the gene products are polypeptides selected from ADR99124 and the gene products are polypeptides selected from ADR99124 and the gene products are polypeptides selected from ADR99124 and the gene products are polypeptides selected from ADR99124 and the gene products are polypeptides selected from ADR99124 and the gene products are polypeptides selected from ADR99124 and its useful for diagnosing became and and disease tissue. M3 is useful for manitoring the response of a breast cancer patient to treatment with an anti-cancer agent. M4 is useful for identifying a compound for treatment with part of the printed specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/bublished_pct_sequences.
 403
 463
 414
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 534
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 594
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 703
 714
 763
 774
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 834
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 943
 954
 YGYVCATKIMKLRKILEKVEAASGFTSEEKDPEBFLNILPHHILRVEPLLKIRSAGGKVQ
 355 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL
 ALFVKLKSCRPDSRFASLOPVSNOIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK
 YGYVCATKIMKLRKILEKVEAASGFTSEEKDPEBFLNILFHHILRVEPLLKIRSAGGKVQ
 DCYFYQIFMEKNEKVGVPTIQQLLEWSFINSNLKFAEAPSCLIIQMPRFGKDFKLFKKIF
 MADROGGONGFNI POVTPCPEVGEYLKMSLEDLHSLDSRRI OGCARRLLCDAYMCMYQSP
 KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEI VNPLRI
 PSLELNITDLLEDTPROCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHPKR
 PSLELNI TDLILEDTPROCRI CGGLAMYECRECYDDPDI SAGKI KOFCKITCNTQVHLAPKR
 LINHKYNPVSLPKDLPDWDWRHGCIPCQNMELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL
 TTENREHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 EVGSLAEVKENPPFYGVIRWIGOPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK
 ALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK
 KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKBKNDVEYYSETQELLRTEIVNPLRI
 LINHKYNPVSLPKDLPDWDWRHGCIPCQNWELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
 TTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 for diagnosing breast
 Gaps
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 Length 960;
 0; Indels
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 present invention relates to a method (M1)
 63.9%; scor.
100.0%; Pred. No. o,
... 0; Mismatches
 DB
 Matches 606; Conservative
 TMSLYK 949
 Query Match
Best Local Similarity
 Sequence 960 AA
 344
 404
 415
 475
 535
 595
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Claim 3; SEQ ID NO 250; 53pp; English

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Query Match
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 antiarthritis, antirheumatic, gastrointestinal-Gen; antiathritis, antirheumatic; antiathritis, antirheumatic; antiathreaty, gastrointestinal-Gen; antiathratic; antiatheraty; gane therapy; immune disorder; usercopic; inflammatory disorder; gane therapy; immune disorder; aperrant apoptosis; hepatic disorder; NF-kappaB regulation; cancer; aberrant apoptosis; hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour; hyper-IgM syndrome; hypohidrotic ectodermal dysplasia; X-linked anhidrotic ectodermal dysplasia; immunodeficiency; viral infection; HIV-1; HTM-1; hepatitis B; hepatitis C; EBV; influenza; viral replication; host cell survival; evasion of immune response;
 770
 470
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 403
 463
 643
 703
 710
 763
 PSLELNITDLLEDTPRQCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHPKR 823
 MADRDGGQNGFNIPQVTPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLLCDAYMCMYQSP 943
 NF-kappaB pathway, antiinflammatory; cytostatic; hepatotropic; virucide;
 ALFVKLKSCRPDSRFASLQPVSNQ1ERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK
 YGYVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRVEPLLKIRSAGQKVQ
 YGYVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRVEPLLKIRSAGQKVQ
 DCYFYQIFMEKNEKVGVPT1QQLLEWSF1NSNLKFAEAPSCL11QMPRFGKDFKLFKK1F
 EVGSLAEVKENPPFYGVIRWIGOPPGLNEVLAGIELEDECAGCTDGTFRGTRYFTCALKK
 DCYFYQI FMEKNEKVGVPTIQQLLEWSFINSNLKFAEAPSCLIIQMPRFGKDFKLFKKIF
 LNHKYNPVSLPKDLPDWDWRHGCIPCONMELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
 411 TTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMBELNTAPVQESPPLAMPPGNSHGL
 KKGI OGHYNSCYLDSTLPCLFAFSSVLDTVLLRPKEKNDVEYYSETOGLLRTEIVNPLRI
 RSELFYTLNGSSVDSQPQSKSKNTWY1DEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL
 351 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL
 TTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 BVGSLAEVKENPPFYGVIRWIGOPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK
 ALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK
 KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRI
 Gaps
 ö
 Length 956;
 0; Indels
 Human NF-kappaB pathway-associated protein SeqID490.
 . 9
sequence represents the human CYLD polypeptide
 63.9%; bcc. 100.0%; pred. No. c,
 ADR14489 standard; protein; 956 AA.
 (first entry)
 Matches 606; Conservative
 TMSLYK 949
 TMSLYK 956
 Similarity
 Sequence 956 AA;
 21-OCT-2004
 344
 Query Mac.
 531
 591
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Thus invention relates to the movel association of protein sequences (and the genes which encode them) to the NF kappaB pathway. The invention may be useful for the production of compounds with an antiinflammatory, cytostatic, hepatotropic, vincide, antiatrhitic, antisthemmatic, gastrointestinal-den, antiatheritic, antisthemmatic, immunodulator, cerebroprotective, antiatrhitic, antisthemmatic, discussed associated with the NF kappaB pathway. The condition is an useful for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NF kappaB pathway. The condition is an immune disorder, an inflammatory disorder, an inflammatory disorder, an inflammatory disorder, an inflammatory disorder, paper celated to aberrant NF-kappaB regulation, cancer, aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas, haematopoletic tumours, hypor-IgM syndromes, hypohidrotic ectodermal dysplasis, immunediciency, viral infections, HIV-1, HILV-1, hepatitis B, hepatitis C, EBW, influenza, viral replication, host cell survival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cacheria, euthyroid sick syndrome, stroke, EAE, autoimmune disorders, disorders related to hypercompenital conditions, birth defects, necrotic lesions, wounds, crypercompenital conditions, birth defects, necrotic lesions, wounds, crypercompenital conditions, birth defects, necrotic lesions, wounds, cryper related to aberrant signal transplant rejection, conditions related to organ transplant conditions in the NP-kappaB pathway of the invention Note This sequence does not appear in the specification but the viruses. The present form the papear in the specification but the viruse of the movel association with the NP-kappaB pathway of the conditions are appear in the specification but appear from conditions.
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 410
 411 TTENRFHSLPPSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL 470
 463
 New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.
rheumatoid arthritis; inflammatory bowel disease; colitis; asthma; atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE; autoimmune disorder; hyper immune activity; aberrant acute phase response; hyperomenial condition; birth defect; necrotic lesion; wound; organ transplant rejection; aberrant signal transduction; proliferating disorder; cancer;
 351 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL
 344 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL
 404 TTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 This invention relates to the novel association of protein sequences
 Gaps
 ;
0
 63.9%; Score 606; DB 8; Length 956;
100.0%; Pred. No. 0;
1ve 0; Mismatches 0; Indels
 Carman J;
 was obtained by the indexer from Genbank
 Claim 6; SEQ ID NO 490; 237pp; English.
 Neubauer MG, Feder JN,
 (BRIM) BRISTOL-MYERS SQUIBB CO.
 13-JAN-2004; 2004WO-US000798
 14-JAN-2003; 2003US-0440068P
 12-MAY-2003; 2003US-0469757P
 Matches 606; Conservative
 HIV propagation; human
 2004-562168/54.
 Similarity
 N-PSDB; ADR14488
 Sequence 956 AA;
 WO2004065577-A2.
 Homo sapiens.
 05-AUG-2004.
 Nadler SG,
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647
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 The invention relates to methods of identifying compounds that alter on more biological activities of CD40. One method involves screening for molecules that modulate the binding of NF-kappaB essential modulator (NEMO) and CYLD. The methods and compositions of the invention of determining compounds that agonize or antagonize a CD40 signaling activity, are useful for the further definition of CD40-mediated signaling pathways, and for manipulation of CD40-mediated cellular responses. They also provide therapeutic agents for treating disorders the immune system, and inflammatory and cancer diseases. The present
 648 YGYVCATKIMICIRKILEKVEAASGFTSEEKDPEEFLNILFHHILIRVEPLLKIRSAGGKVQ
PSLELNI TDLLEDTPRQCRI CGGLAMYECRECYDDPDI SAGKIKQFCKTCNTQVHLHPKR
 DCYFYQI FMEKNEKVGVPT1QQLLEWSF1NSNLKFAEAPSCL11QMPRFGKDFKLFKKIF
 LINHKYNPVSLPKDLPDWDWRHGCIPCQNMELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
 MADRDGGQNGFNI PQVTPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLLCDAYMCMYQSP
 PSLELNITDLLEDTPROCRICGGLAMYECRECYDDPDISAGKIKOFCKTCNTQVHLHPKR
 Identifying compounds that alter one or more biological activities of CD40 by modulating the binding of NEMO and CYLD, useful for treating disorders of the immune system, and inflammatory and cancer diseases.
 CD40; NF-kappaB essential modulator; NEMO; CYLD; immunosuppressive; antiinflammatory; cytostatic; gene therapy; human.
 Dougall WC;
 Claim 1; Page 38-44; 48pp; English.
 ABB82783 standard; protein; 956 AA.
 07-MAY-2002; 2002WO-US014570.
 08-MAY-2001; 2001US-00851673.
 (first entry)
 Derry JMJ, Fanslow WC,
 Human CYLD polypeptide
 (IMMV) IMMUNEX CORP
 WPI; 2003-120669/11.
 948 TMSLYK 953
 TMSLYK 949
 N-PSDB; ABV75394
 WO200292761-A2.
 18-MAR-2003
 Homo sapiens
 21-NOV-2002.
 588
 708
 768
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 888
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 ABB82783
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 467
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 584 KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRI 643
 The invention relates to purified proteins and genes encoding them, that are involved in T cell activation (I) and has an amino acid deletion, substitution or addition in the amino acid sequences. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of autoimmune disease (rheumatoid arthritis, asthma, multiple sclerosis and diabetes), allergic disease, infections disease, AIDS, and acute or chronic respection at organ transplant or bone marrow transplant. This sequence corresponds to a protein involved in T
 New purified protein involved in T cell activation, useful for diagnosing, preventing and/or treating acquired immunodeficiency syndrome, autoimmune (e.g. rheumatoid arthritis, and diabetes), allergic
 BVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDBCAGCTDGTFRGTRYFTCALKK
 antiallergic; antiarthritic; antiasthmatic; antidiabetic; anti-HIV; antimicrobial; antirheumatic; immunosuppressive; neuroprotective; gene therapy; T cell activation; diagnosis; autoimmune disease; rheumatoid arthritis; asthma; multiple sclerosis; diabetes; allergic disease; infectious disease; AIDS; chronic rejection; organ; bone-marrow transplant.
 344 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL
 TTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 TTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAOSVMEELNTAPVOESPPLAMPPGNSHGL
 EVGSLAEVKENPPFYGVIRWIGOPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK
 ALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK
 ALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK
 Gaps
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0
 8; Length 953;
 0; Indels
 DB 7
 100.0%; Prec. ...
 cell activation associated protein #48.
 63.9%; Score 606;
 Claim 1; SEQ ID NO 96; 2828pp; English
 (ASAH-) ASAHI KASEI PHARMA CORP
 2002JP-00376365.
2002US-0436473P.
2003JP-00122113.
 28-APR-2003; 2003US-0465792P.
21-OCT-2003; 2003JP-00360559.
22-OCT-2003; 2003US-0512846P.
 2003WO-JP016715
(first entry)
 Conservative
 and infectious diseases.
 Matsuda A, Yoneta S;
 2004-593134/57.
 al Similarity
606; Conserv
 N-PSDB; ADQ95917
 Sequence 953 AA;
 activation.
 WO2004058805-A2.
 Homo sapiens
 25-DEC-2003;
 25-APR-2003;
 07-OCT-2004
 15-JUL-2004
 348
 404
 408
 464
 468
 528
 Query Match
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Sequence 953 AA;
 TMSLYK
 888
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 648
 708
 768
 404
 464
 468
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 704
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 828
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 944
 948
 AD095918;
 524
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 Query Match
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 RESULT 5
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 The invention relates to breast specific polypeptides (BSPB) and nucleic acids (breast specific nucleic acids; BSNAs) encoding them. The invention also relates to vectors and host cells comprising a BSNA sequence; antibodies against BSPB; the recombinant production of BSPB; methods of detection of BSNAs or BSPB in a sample); kits for detecting a risk of cancer or presence of cancer in a patient; and vaccines comprising a BSNA or BSP. The invention additionally discloses fragments, mutants, fusion
 non-cancerous
433
 493
 763
 553
 823
 883
 673
 943
 733
 Human; breast specific polypeptide; BSP; breast specific nucleic acid; BSNA; breast cancer; metastasis; non-cancerous disease; breast tissue; identification; monitoring; diagnosis; enginees breast tissue production; transgenic animal; drug screening; cytostatic; gene therapy; vaccine; chromosome 16p13.3.
 MADROGGONGFNI POVTPCPEVGEYLKWSLEDLHSLDSRRIOGCARRLLCDAYMCMYOSP
 MADRDGGQNGFNI PQVTPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLLCDAYMCMYQSP
 DCYFYQIFMEKNEKVGVPTIQQLLEWSFINSNLKFAEAPSCLIIQMPRFGKDFKLFKKIF
 PSLELNITDLLEDTPRQCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHPKR
 LINHKYNPVSLPKDLPDWDWRHGCIPCQNMELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
 LNHKYNPVSLPKDLPDWDWRHGCIPCQNWELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRI
 YGYVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRVEPLLKIRSAGQKVQ
 DCYFYQIFMEKNEKVGVPT1QQLLEWSF1NSNLKFAEAPSCL11QMPRFGKDFKLFKK1F
 PSLELNITDLLEDTPROCRICGGLAMYECRECYDDPDISAGKIKOFCKTCNTQVHLHPKR
 breast specific polypeptide useful for identifying, diagnosing, toring, staging, imaging and treating breast cancer and non-car
 Human breast specific polypeptide (BSP) DEX0238_137, SEQ ID NO:137
 Disclosure; SEQ ID NO 137; 264pp; English.
 Ä
 ADC24816 standard; protein; 953
 29-AUG-2002; 2002WO-US027777
 31-AUG-2001; 2001US-0316306P
 ŝ
 (first entry)
 monitoring, staging, imadisease states in breast
 Liu C, Salceda
 (DIAD-) DIADEXUS INC.
 2003-290182/28.
 739
 TMSLYK 949
 N-PSDB; ADC24898
 WO2003020900-A2
 Homo sapiens
 18-DEC-2003
 13-MAR-2003
 674
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proteins, homologous proteins and allelic variants of BSPB; methods for identifying and designing agonists and antagonists of BSPB; methods for identifying and monitoring breast tissue; producing engineered breast tissue for tissue for treatment and research; producing transgenic animals and cells comprising BSNA sequences; aptamers evolved to bind specifically to BSPB; and single exon probes based on BSNA sequences BSPB, BSNAB and cands single exon probes based on BSNA sequences in BSPB and Cantering, staging, imaging and treating breast cancer (including breast concernetsates), and non-cancerous disease states in breast tissue. Cancer metastases), and non-cancerous disease states in breast tissue. BSPB and BSNAB may additionally be used to identify and monitor breast concerned breast tissue for treatment or research. BSNAB production of engineered breast tissue for treatment or research. BSNAB can and salso be used in gene therapy and in the production of transgenic animals and cells. The present sequence represents a breast specific polypeptide (BSP) disclosed in the invention.
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 467
 643
 703
 883
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 527
 587
 707
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 DCYFYQIFMEKNEKVGVPT1QQLLEWSFINSNLKFAEAPSCL11QMPRFGKDFKLFKKIF
 ALFVKLKSCRPDSRPASLOPVSNOIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK
 LMHKYNPVSLPKDLPDWDWRHGCIPCQNWELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
 MADRDGGONGFNIPOVTPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLLCDAYMCMYQSP
 344 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL
 348 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL
 408 TIENRFHSLPFSLIKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 EVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK
 KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRI
 DCYPYQIFMEKNEKVGVPT1QQLLEWSPINSNLKFAEAPSCL11QMPRFGKDFKLFKKIF
 MADRDGGONGFNIPOVTPCPEVGEYLKMSLEDLHSLDSRRIGGCARRLLCDAYMCMYQSP
 TTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 EVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK
 ALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK
 YGYVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRVEPLLKIRSAGQKVQ
 PSLELNITDLLEDTPRQCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHPKR
 LNHKYNPVSLPKDLPDWDWRHGCIPCONMELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
 KKGI QGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEI VNPLRI
 Gaps
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 DB 7; Length 953;
0;
 0; Indels
 100.0%; Pred. No. 0; ive 0; Mismatches
 Score 606;
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 ADQ95918 standard; protein; 953
 63.98;
 al Similarity 100.
606; Conservative
 TMSLYK 949
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2000US-0232398P.
 2000US-0235834P,
2000US-0235836P,
 2000US-0240960P
 000US-0241787P
 2000US-0249215P
 000US-0236802P
 0000US-0244617P
 2000US-0249265P
 000US-024
 000US-02
08-SEP-2000; 2
08-SEP-2000; 2
08-SEP-2000; 2
12-SEP-2000; 2
14-SEP-2000; 2
14-SEP-2000; 2
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14-SEP-2000; 2
 14-SEP-2000; 2
14-SEP-2000; 2
14-SEP-2000; 2
21-SEP-2000; 2
21-SEP-2000; 2
25-SEP-2000; 2
 01-NOV-2000; 208-NOV-2000; 208
 -SEP-2000;
-SEP-2000;
-SEP-2000;
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-SEP-2000;
 -OCT-2000;
-OCT-2000;
 -OCT-2000;
-OCT-2000;
-OCT-2000;
-OCT-2000;
 -SEP-2000;
 -OCT-2000;
 SEP-2000;
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The present invention relates to the isolation of novel human enzyme polypeptides, and the CDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. ALDS) autoimmune disorders (e.g. atheritis), neurological disorders (e.g. ALDS) autoimmune disorders (e.g. atheritis), neurological disorders (e.g. ALDS) autoimmune disorders (e.g. atheriar's disorders (e.g. atheriar) and infectious disorders (e.g. atherosclerosis), blood-related disorders (e.g. influence).

Cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. influence).

Cardiovascular disorders (e.g. influence). The polynuclectides of the invention can also be used in gene therapy. AAU22915-AAU23814 represent the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL 193
 Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
 ALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK
 TIENRFHSLPFSLIKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 EVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK
 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPVNSL
 TTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 EVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK
 Gaps
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0
 Ouery Match 63.9%; Score 606; DB 4; Length 739; Best Local Similarity 100.0%; Pred. No. 0; Matches 606; Conservative 0; Mismatches 0; Indels
 Claim 11; SEQ ID NO 1743; 1180pp; English
 Rosen CA, Barash SC, Ruben SM;
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-025103P.
05-DEC-2000; 2000US-025103P.
05-DEC-2000; 2000US-025109P.
06-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-025199P.
 05-JAN-2001; 2001US-0259678P
 HUMAN GENOME SCI INC
 WPI; 2001-465566/50
 N-PSDB; AAS41617
 Sequence 739 AA;
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KKGIQGHYNSCYLDSTLRCLPAFSSVLDTVLLRPKEKNDVBYYSETQELLRTEIVNPLRI

AAU23747 standard; protein; 739 AA.

(first entry)

17-DEC-2001

AAU23747;

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RESULT 3
AAU23747
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 AAY91946-61 show human cytoskeleton associated proteins 1 to 16 (CYSKP-1 to CYSKP-16) respectively. The sequences can be used to treat and diagnose cancer and cell proliferative, autoimmune/inflammatory, vesticle trafficking, neurological, cardiovascular, cell motility, reproductive and muscle disorders. Pharmaceutical compositions containing CYSKP-2 to CYSKP-16 can be used to treat or prevent disorders associated with decreased expression or activity of CYSKP (claimed), for example, atherosclerosis, cirrhosis, hepatitis, myelofibrosis, psoriasis, autoimmune/antiinflammatory disorders such as allergies, anemia, asthma, acquired immunodeficiency syndrome (AIDS), Crohn's disease, diabetes mellitus, Goodpasture's syndrome, osteoarthritis, scleroderma and trauma. CYSKP antagonists can be used to treat or prevent a disorder associated with increased expression or activity of CYSKP (claimed)
 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL 185
 943
 344 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL 403
 463
 305
 583
 365
 643
 425
 703
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 763
 545
 823
 605
 883
 Human cytoskeleton associated proteins, used to treat cell proliferative, autoimmune/inflammatory, vesicle trafficking, neurological, cell motility, reproductive and muscle disorders.
 EVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK
 ALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK
 YGYVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRVEPLLKIRSAGQKVQ
 EVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK
 ALFVKLKSCRPDSRPASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK
 YGYVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRVEPLLKIRSAGQKVQ
 DCYFYQI FMEKNEKVGVPTIQQILEWSFINSNLKFAEAPSCLI I OMPRFGKDFKLFKKI F
 TTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 TTENRFHSLPFSLTKOPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
 PSLELNITDLLEDTPROCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHPKR
 LNHKYNPVSLPKDLPDWDWRHGCIPCQNMELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
 LNHKYNPVSLPKDLPDWDWRHGCIPCQNMELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
 MADRDGGQNGFNI PQVTPCPBVGEYLKMSLEDLHSLDSRRIQGCARRLLCDAYMCMYQSP
 KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRI
 DCYFYQIFMEKNEKVGVPT1QQLLEWSFINSNLKFAEAPSCL11QMPRFGKDFKLFKKIF
 Gaps
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 63.9%; Score 606; DB 3; Length 731;
 Indels
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 100.0%; Preu. ...ive 0; Mismatches
 Claim 1; Page 91-93; 113pp; English.
 Local Similarity 100.
Hes 606; Conservative
WPI; 2000-283582/24
N-PSDB; AAA08589.
 TMSLYK 949
 TMSLYK 731
 Sequence 731 AA;
 126
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| Movel | human coxidoredurase enzyme | transferase; hydrolase; lyase; isomerase; | Maintain, oxidoredurase enzyme; | transferase; hydrolase; lyase; isomerase; | Maintain, oxidoredurase enzyme; | transferase; hydrolase; lyase; isomerase; | Maintain, oxidoredurase; | manunodéficiany disorder; | manunodéficiany disorder; | minitainment disorder; | manunodéficiany disorder; | minitainment odisorder; | manunodéficiany disorder; | minitainment odisorder; | manunodéficiany disorder; | minitainment odisorder; | manunodéficiany disorder; | minitainment ```

74.74

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19-JUL-2000 (first entry)
                          immunosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amycrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, archer disposses and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
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                 invention relates to human nucleic acids (AAI57798-AAI61369) and the
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ive 0; Mismatches
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Matches 606; Conservative
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AAY91954 standard; protein; 731 AA.

RESULT 2
AAY91954
ID AAY9
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AC AAY9

AAY91954;

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Cytoskeleton associated protein; CYSKP-9; cancer; proliferative; autoimmunity; inflammatory, vesicle trafficking; neurological; cardiovascular; cell motility; reproductive; muscle disorder.
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Baughn MR;
                             Human cytoskeleton associated protein 9 (CYSKP-9)
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Guegler KJ, Patterson C,
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27-APR-1999;
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                                                                                                                                        Domain
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us-09-671-687a-3.0ligo.rag

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5.1.6
Compugen Ltd
GenCore version
Copyright (c) 1993 - 2005
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protein search, using sw model OM protein

Run on:

April 18, 2005, 09:14:43; Search time 73 Seconds (without alignments) 5027.885 Million cell updates/sec

US-09-671-687A-3 949

Title: Perfect score:

1 MSSGLWSQEKVISPYWEERI......RLLCDAYMCMYQSPIMSLYK 949 Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

2105692 seqs, 386760381 residues Searched:

0 Word size

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

A_Geneseq_16Dec04:* Database :

geneseqp1990s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003s:* geneseqp2003bs:* geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ID Description	AAM39254 Human pol	AAY91954 Human Cyt	Novel	Human	ADQ95918 ADQ95918 T cell ac		ADR14489 Human NF	ADR99244 DKFZp586D	Aab95828	ADQ95916 Adq95916 T cell ac	ADQ95920 T cell ac	AAM41040 Aam41040 Human pol	AAB95719 AAB95719 Human pro	AAU23211 Novel hum	ABB89233 Human pol	ABB89234 Human pol	ರ	ABB33941 Peptide	AAM27399 Peptide	ABB28754 Peptide	ABB19377 Protein (AAM67104 Aam67104 Human bon	AAMS4704 Human bra	AAM02691	ABCOCACA District Abcocaca account
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ALIGNMENTS

AAM39254 standard; protein; 685 RESULT 1 AAM39254

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AAM39254;

(first entry) 22-OCT-2001 Human polypeptide SEQ ID NO 2399.

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; harease; harease; harease; harease; harease; harease; harease; harease; harease; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

Homo sapiens.

leukaemia.

WO200153312-A1.

26-JUL-2001.

26-DEC-2000; 2000WO-US034263.

21-JAN-2000; 2000US-00488725. 25-APR-2000; 2000US-00552317. 20-JUN-2000; 2000US-0055317. 19-JUL-2000; 2000US-00653450. 13-AUG-2000; 2000US-00653450. 14-SEP-2000; 2000US-00653450. 19-OCT-2000; 2000US-00693036. 29-NOV-2000; 2000US-00727344. 99US-00471275 23-DEC-1999;

(HYSE-) HYSEQ INC.

ę o Wang D; , Zhao Q Ren F, Wa Qian XB, Yang Y, Liu C, Asundi V, Chen R, Ma Y, Wang Z, Wehrman T, Xu C, Xue AJ, Goodrich R, Drmanac RT; Tang YT, Wang J, 1 Zhou P, (

WPI; 2001-442253/47. N-PSDB; AAI58410. Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

Example 4; SEQ ID NO 2399; 10078pp; English

us-09-671-687a-3.0ligo.rst

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Bases I to 349; Primates; Catarrhini; Hominidae; Homo. 1 (Bases I to 349; Primates; Catarrhini; Hominidae; Homo. 2 Shang, C.H., Ye, M., Wu, X.Y., Ren, S.X., Zhao, M., Zhao, M., Zhao, M., Zhao, M., Zhao, M., Zhao, J., Hangarg, C.H., Zhou, J., Hu, G.X., Gu, J., Chen, S.J. and Chen, Z. Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells
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3 (bases 1 to 3496)
Zhang,Q.H., Ye,M., Zhou,J., Shen,Y., Wu,X.Y., Guan,Z.Q., Wang,L., Fan,H.X., Mao,Y.E., Dai,M., Huang,Q.H., Chen,S.J. and Chen,Z.
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HT161542.1 GI:6841351
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AA152263
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               GenCore version Copyright (c) 1993 - 2005
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Clark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritera, S., Wango, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                          462 GlyLeuGluValGlySerLeuAlaGluValLysGluAsnProProPheTyrGlyVallle
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                                                                                                                    422 ThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGlnSerValMetGluGlu
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Homo sapiens CYLD gene, VIRTUAL TRANSCRIPT, partial sequence,
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[1 (bases 1 to 2862)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Rerriera, S., Wango, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
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This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
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Mammalia; Buthoria; Primates; Catarrhini; Hominidae; Homo.
El (bases 1 to 1039)
NIH-MGC http://mgc.noi.nih.gov/.
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Llocation/Qualifiers
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       1579 AAGGCGCTGTTTGTGAAAACTGAAGAGCTGCAGGCCTGACTCTAGGTTTGCATCATTGCAG
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                                       Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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Matches:
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Mismatches:
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/organism="Pan troglodytes"
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Science 302 (5652), 1960-1963 (2003)
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Gaps:
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RCE Homo sapiens (human) RGANISM Homo sapiens Bukaryota; Metazoa; Chordat Mammalia; Eutheria; Primate BUTO 1063) I (bases 1 to 1063) ITLE NATIONAL INTERNOTE STAUSDERGY Email: Cgapbs-r@mail.nih.gc Tissue Procurement: ArCayed by: T CDNA Library Arrayed by: T CDNA Library Arrayed by: T CDNA Library Arrayed by: T CONA LIBRARY ARRAYED CONA LIBRARYED CONA LIBRA	Gaps:
ery Match: 4	Qy 727 LeuGlUTTPSerPhelleAsnSerAsnleeLysPheAlaGluAlsProSerCysLeulle 746 Db 554 TTACAATGGTCTTTTATCAACAGGAACTGAAATTTGCAGAGGCACCATGTTGATT 613 Qy 747 IleGlMACTPTTATCAACCTGAAATTTGCAGAGCACCATGTTGATT 613 Qy 747 IleGlMACTPTATCAGAACTGTAAACTTGAAAAATTTTCCTTCTTGTG 673 Qy 747 IleGlMACTPTAACAGAACTTAAAATTTAAAAAATTTTCCTTCTTTTCTTTC

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

E. (bases 1 to 677) Homo.

E. (bases 1 to 677) Yang, J., Au-Young, J. and Stuve, L.L.

Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

Contact: Fu GK

Incyte Genomics 84 (1), 205-210 (2004)

Contact: Fu GK

Incyte Genomics, Inc.

3160 Porter Dr., Palo Alto, CA 94304, USA

Tel: 6508454102

Email: gfu@incyte.com.

Location/Qualifiers

10.677
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                                                                                                                                     CysTyrPheTyrGlnIlePheMetGluLysAsnGluLysValGlyValProThrIleGln 724
                                                                                                                                                                                                                              GluGluAsnThrProProLysMetGluLysGluGlyLeuGluIleMetIleGlyLysLys
                                                                                                                                                                                                                                                      122 GAAGAAAATACTCCACCAAAAAAGAAAAAGAAGGCCTGGAGATAATGATTGGGAAGAAG
                                                                                                                                                                                                                                                                                                                                               AlaSerGlyPheThrSerGluGluLysAspProGluGluPheLeuAsnIleLeuPheHis
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                                                                                                                                                                                                                                                                                                                   LysG1y11eG1nG1yHisTyrAsnSerCysTyrLeuAspSerThrLeuDheCysLeuPhe
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                                              LeuPheValLysLeuLysSerCysArgProAspSerArgPheAlaSerLeuGlnProVal
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56076837J1 FLP Homo sapiens CDNA, mRNA sequence.
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    US-09-671-687A-3 (1-949) x CR772310 (1-726)
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Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
1. 726
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/dev_stage="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost
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DKFZp468L0123_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone
DKFZp468L0123_5', mRNA sequence.
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This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKF2);
Email s.wiemann@dkfz-heidelberg.de; any. Please contact RZPD for
                                              480
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pongo.
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Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   et al.)
                                                                                                                                                                                                                                                                                                                                                          SerGluGluLysAspProGluGluPheLeuAsnIleLeuPheHisHisIleLeuArgVal
                                                                                                                GluProLeuLeuLysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGln
                                                                                                                                                                                                                                                                      11ePheMetGluLysAanGluLysValGlyValProThr11eGlnGlnLeuLeuGluTrp
                                                                                                                                                                                                                                                                                                  601 ATTTTATGGAAAAAAATGAGAAAGTTGGCGTTCCCACAATTCAGCAGTTGTTAGAATGG
ThrLysIleMetLysLeuArgLysIleLeuGluLysValGluAlaAlaSerGlyPheThr
                         ACAAAAATTATGAAACTGAGGAAAATACTTGAAAAGGTGGAGGCTGCATCAGGATTACC
                                                                                                                                                                                                                         GAACCTITIGCTAAAATAAGATCAGCAGGTCAAAAGGTACAAGATTGTTACTTCTATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pongo pygmaeus mRNA (Poustka,A., Albert,R., Moosmayer,P.,
Unpublished (2004)
Contact: MIPS
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684 481 704 541 601 744 661

644

604 241 624

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/clone_lib="U1-E-E01"
/lab host="DH2"
/lab host="DH2"
/lab host="DH3"
/lab host="D
                                                                                                                                                                                                                     University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA TTel: 319 318 8250
Fax: 319 319 355 855
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             781
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                                Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                          Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
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1. .697
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Seq primer: M13 Reverse.
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          (bases 1 to 697)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             611 AATCCTCTGAGAATATATGGATATGTGTGTGCGCACAAAATTATGAAACTGAGGAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuGluLygValGluAlaAlaSerGlyPheThrSerGluGluLygAspProGluGluPhe
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BM724143
BM724143.1 GI:19045474
EST.
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Homo sapiens
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CR789083 601 bp mRNA linear EST 01-OCT-2004 DKFZp468Ll332_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone DKFZp468Ll332_5', mRNA sequence.
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This is the 5' sequence of the clone insert. Clone from S. Wiemann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   542 TTAGCATTTGGAGGCTACTTAAGTGAAGTAGTAGAAGAAAATACTCCACCAAAAATGGAA 601
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Ansorge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B., Mewes, H.W., Weil, B., Amid, C., Oganger, A., Fobo, G., Han, M. and Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pongo pygmaeus mRNA (Ansorge,W., Krieger,S., Regiert,T., et al.)
Unpublished (2004)
Contact: MIPS
                                                                                                                                                                                                                       CCACTCCACTCCTCTGTGAACTCACTGACCACGAGAAACAGATTCCACTTTACCA
                                                                                                                                                                                                                                                                       PheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeu
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                                                                                                                                                                                                                                                                                             TTCAGTCTCACCAAGATGCCCAATAGCAATGGAAGTATTGGCCACAGTCCACTTTTTTG
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                                                                                                                            374 AlaGluAspProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerPro
                                                                                                                                                GCAGAAGACCCTGCAAAAATCTCTTACAGAGATATCTACAGAGTTTGACCGTTCTTCACCA
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Mismatches:
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Gaps:
                                                                                        US-09-671-687A-3 (1-949) x CN335014 (1-624)
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Pongo pygmaeus
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 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Contact: Brandenberger R
Regenerative Medicine
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 624)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
                                 882 AspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIleProGlnValThrPro
                                                                                                                                                                            ThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSerAlaTrpLeuPhePhe
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                                                                                                                                                                                                                                                                                                                                             498 TGCCCAGAAGTAGGAGAGTACTTGAAGATGTCTCTGGAAGACCTGCATTCCTTGGACTCC
198 TCAGCTGGAAAATCAAGCAGTTTTGTAAAACCTGCAACACTCAAGTCCACCTTCATCCG
                                                                                                       TrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAlaValLeuCysIleGlu
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17000531936046 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
CN335014
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230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
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/mol_type="mRNA"
/db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: rbrandenberger@geron.com
Insert Length: 624 Std Error:
    Location/Qualifiers
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                                                                                                                                                              /clone="DKKZD46811332"
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                                          http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp468L1332
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
Molecular Genome Analysis, German Cancer Research Center (DKPZ);
Email s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact
RZPD for ordering:
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Mismatches:

    .601
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/mol_type="mRNA"
    /db_xref="taxon:9600"

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of 10 nucleotides with a PHRED quality not less than 20. A terminal stretch of at most 40 un-masked bases were automatically trimmed when flanking masked sequence. Sequences with an INTERNAL continuous stretch of at most 20 bases with PHRED quality less than 20 were automatically prepared for submission. HiQUAL START and HIQUAL STOP refer to the coordinates on CLIP_QUALITY and CLIP_VECTOR at the
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                        below:
                                                                                                                   Dvorak, C.M.T., Hyland, K.A., Zhang, Y., Fahrenkrug, S.C. and
                                                                                                                                               Porcine jejunal Peyer's patch expressed sequences Unpublished (2003)
                                                                                                                                                                                                                  1971 Commonwealth Ave., St. Paul, MN 55108,
                                                                                                                                                                         Contact: Murtaugh, M.P.
Department of Veterinary PathoBiology
University of Minnesota
                                                                 Sus scrofa
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                        Email: murta001@umn.edu
                          GI:28577807
                                                                                                        (bases 1 to 596)
                                                                                                                                                                                                                                                                         quality
                                                                                                                                                                                                                                 Tel: 612-625-6735
                                                                                                                                                                                                                                             Fax: 612-625-5203
                                                      Sus scrofa (pig)
                                                                                                                                 Murtaugh, M.P.
sequence.
CB286853
CB286853.1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

B. 1 (basea 1 to 575)
S. Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

L. Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: yeuzukieims.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                       BP226285
BP226285 Sugano cDNA library, dermoid cancer Homo sapiens cDNA
Clone DMC02192, mRNA sequence.
BP226285
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                                                                                                 GTAGAACCATTGTTAAAAATAAGATCAGCAGGTCAAAAAGTACAAGATTGTTACTTCTAT
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                           ACCTCTGAAGAAAAAGATCCTGAAGAATTTTTGAATATCCTGTTTCATCATATTTTAAGG
                                                                     ValGluProLeuLeuLysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyr
                                                                                                                                                                                                                                                  729 TrpSerPheIleAsnSerAsnLeuLysPheAlaGluAlaProSerCysLeu 745
                                                                                                                                                                                                                                                                              544 TGGTCTTTTATCAACAGTAACCTGAAATTTGCGGAGGCACCATCATGTCTG 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Sugano cDNA library, dermoid cancer"
/note="dermoid cancer"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                               /do xere="reson:9823"
/clone="PSGUBLIB 32807"
/tissue type="Peyer's patch"
/clone lib="UnwinkPM3"
/note="Organ: small intestine, jejunum; Vector:
pcWVSPORT6; Site 1: Not1; Site 2: Sal1; Jejunal Peyer's
patches were isolated from healthy, 4-6 week old
cross-bred pigs. RNA was extracted either immediately or
after 3 hours stimulation in an Ussing chamber with one of
the following treatments: 1) no treatment, 2) Salmonella
choleraesuis vaccine strain SC-54, 3) phorbol myristeate
actete, concanavalin A, and 8-bromo-cyclic AMP, and 4)
lipopolysaccharide and cholera toxin. Each treatment was
performed in the presence and absence of cycloheximide.
Purified poly A + RNA from each of the treated tissues
(2-4) was combined together, reverse transcribed, and
cloned in to pcWVSPORT6 to make a library of approximately
530,000 recombinant clones with an average insert size of
1.0 kbp. Poly A+ RNA from freshly isolated and non-treated
tissue from an Ussing chamber (treatment 1) was cloned in
the same manner to produce an unstimulated cDNA library of
approximately 900,000 clones with an average insert size
of 1.5 kbp. Equal portions of the two libraries were
pooled and then subtracted with porcine ST fibroblast RNA
to create a subtracted worth a average insert size of
1.0 kbp."
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NCBI trace archive.
Plate: 32 row: E column: 07
Seq primer: SP6 primer
High quality sequence start: 61
High quality sequence stop: 283.
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/mol_type="mRNA"
/db_xref="taxon:9823"
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CD641429
AGENCOURT_14532010 NIH MGC_191 Homo sapiens cDNA clone
IMAGE:30418040 5', mRNA sequence.
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NIH-MGC http://mgc.noi.nih.gov/.
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       For
sequence tags for this library are GA, AGGAA. additional information, contact: Bento Soares, bento-soares@ulowa.edu
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TAG_SEQ=GA"
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/ organism="Homo sapiens"

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/ db_xref="taxon:9606"

/ clone="UI-1-BC1-ajd-e-08-0-UI"

/ tissue_type="Placenta"

/ tissue_type="BLS | tissue | tissu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Brown
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seg primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF528626
UI-1-BC1-ajd-e-08-0-UI.s1 NCI CGAP_P12 Homo sapiens cDNA clone
UI-1-BC1-ajd-e-08-0-UI 3', mRNA sequence.
                                                                             307
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 581)

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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                              LeuSerLeuSerAlaGlnSerValMetGluGluLeuAsnThrAlaProValGlnGluSer
                                                                             criricicroscoccagicidaaragaagagciaaacacrocaccorccaagaggr
                                                                                                                             ProProLeuAlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGlu
                                                                                                                                                                            308 CCACCCTTGGCCATGCCTCCTGGGAACTCACATGGTCTAGAAGTGGGCTCATTGGCTGAA
                                                                                                                                                                                                                            ValLysGluAsnProProPheTyrGlyValileArgTrpileGlyGlnProProGlyLeu
                                                                                                                                                                                                                                                                            GITAAGGAGAACCCICCITICTAIGGGGIAAICCGIIGGAICGGICAGCCACCAGGACIG
                                                                                                                                                                                                                                                                                                                           AsnGluValLeuAlaGlyLeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThr
                                                                                                                                                                                                                                                                                                                                                  428 AATGAAGTGCTCGCTGGACTGGAACTGGAAGATGAGTGTGCAGGCTGTACGGATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                        PheArgGlyThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                              531 SerCysArgProAspSerArgPheAla 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              548 AGCTGCAGGCCTGACTCTAGGTTTGCA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Unpublished (1997)
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AUTHORS
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460 565

585 400 605 625 280 645 220 999 160

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
El (bases 1 to 919)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Longublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CONA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://mage.llnl.gov
Plate: LLMM.0185 row: e column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Lissue_type="adenocarcinoma, cell line"
/Lab host="DH10B (phage-resistant)"
/Lab host="DH10B (phage-resistant)"
/Lab host="DH10B (phage-resistant)"
/Lab host="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally, oligo-dT primed.
Site_2: SalI; Cloned unidirectionally, oligo-dT primed.
Site_1: Insert size_1.4 kb. Library enriched for full:length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                BG180100 919 bp mRNA linear EST 06-FEB-2001
                                                                                   617
                                   361 GAGATAATGATTGGGAAGAAGAAGAAGGCATCCAGGGTCATTACAATTCTTGTTACTTAGAC 420
                                                                                                            540
                                                                                                                                                                     LysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGluIle 637
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                                                                                      SerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArgPro
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/db_xref="taxon:9606"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-671-687A-3 (1-949) x BG180100 (1-919)
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179.00
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                                                                                                                                                                                                                                                         638 ValAsnProLeuArg 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BG180100
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Best Local Similarity:
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  578
                                                                                      598
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DB:
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AUTHORS
TITLE
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BG180100
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                                                                                                                                                                                                                                                                                                                                                                          /mol type="memory baptens"
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Site 2: Sfil (ggcgctcggcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Monourclear Cells. RNA was pooled from 3/6hour stimulation with PMA adm lonomycin. 5' and 3' adaptor sequence:
S'-ATTCTAGGCGCTATTGGCC-3' and 3' adaptor sequence:
S'-ATTCTAGGCGCGGGGGCGGCGATG-dT (30) BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69
Kb (tange 0.70-5.0 kb). 1.5/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Fallo Alto, CA). Note: This is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyrPhe 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrCysAlaLeuLysEysAlaLeuPheValLysEeuLysSerCysArgProAspSerArg 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGlyLeu 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCTGTGCCCTGAAGAGGCGCTGTTTGTGAAACTGAAGAGCTGCAGGCCTGACTCTAGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
           Context: Daniels S. Gerhard, Ph.D.
Context: Daniels S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIP
Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Proturement: Narayan Bhat
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: NDCM220 row: g column: 09
High quality sequence stop: 584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 GlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGAACTCACATGGTCTAGAAGTGGGCTCATTGGCTGAAGTTAAGGAGAAACCCCTCCTTC
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Matches:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                         1. .736
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
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Search completed: April 17, 2005, 11:37:04 Job time : 6214 secs

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5.1.6
Compugen Ltd.
 version 5
- 2005 (
GenCore
Copyright (c) 1993
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protein search, using sw model OM protein Run on:

April 18, 2005, 09:17:58 ; Search time 22 Seconds (without alignments) 4150.441 Million cell updates/sec

US-09-671-687A-3 949 Title: Perfect score:

1 MSSGLWSQEKVTSPYWEERI......RLLCDAYMCMYQSPTMSLYK 949 Sequence:

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

283416 segs, 96216763 residues Searched:

0

Word size :

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR 79:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	F40F12.5 protein -	protein F40F12.5 [transcription regu	probable transcrip	hypothetical prote	glucose-6-phosphat	glucose-6-phosphat	protein R09B5.1 [i	yaiT protein precu	cytochrome P450 1A	probable membrane	probable AMP-bindi	hydrogenase expres	ribonuclease - Dei	hypothetical prote	_			hypothetical prote	m	neurokinin B precu	probable tail comp			probable ribonucle	hypothetical prote	probable olfactory	hypothetical prote	epithelial membran
	E .	S42834	F88568	865996	C83149	T15188	AG1370	AE1740	D88950	C64765	JS0746	S63361	G83395	E69420	F75530	T33893	A71570	G97134	C97140	T13628	I65342	A43779	T09268	C82665	D71911	AI0448	A84303	S58012	AD1590	JC5045
	B :	7	0	~	7	~	~1	~	N	N	~	0	N,	~	~	~	7	7	~	7	7	7	7	~	0	N	N	0	~	~
	Match Length	727	1021	150	215	448	450	450	458	486	524	551	651	740	760	1086	20	72	81	104	116	116	123	126	143	152	152	157	159	163
* Query	Match	1.3	1.3	0.8	9.0	0.8	0.8	0.8	0.8	0.8	0.8	0.8	•	0.8	0.8	0.8	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7
	Score	12	12	ω	œ	α)	80	80	80	80	80	80	89	ω	œ	80	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Result	No.	1	7	m	4	Ŋ	9	7	۵	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

169 2 C91130 169 2 C85975 171 2 A65103 174 2 A65106 177 2 F96739 178 2 AF578 189 2 A69387 189 2 A90852 189 2 A90852 189 2 A90852 189 2 A90852 189 2 A90852 189 2 A90852	hypothetical prote	pts system, n-acer conserved hypothet neuromedin U precu	hypothetical prote transcription regu hypothetical prote	fumarase (fum-1) h probable antirepre	antirepressor prot antirepressor prot		probable antirepre probable antirepre
0000147800000000000000000000000000000000	C91130 C85975	A65103 E95002 A45356	F96739 A75578 AF1362	A69387 F90780	E90820 A90852	E90874 A90902	B90911 G90999
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	310	3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	3 3 3 4 4	. 8 6 8 7	40 41	42 43	4 4 4 5

ALIGNMENTS

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C.Species: Caenorhabditis elegans
C.Jotte: 20. Peb-1995 #text_change 24-Nov-1999
C.Jotteshaw, J. S42834
A.Jottes Dealiminary
A.Jottes: Species preliminary
A.Jottes: preliminary
A.Jottes: preliminary
A.Jottes: DNA
A.
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Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    856 AVLCIETSHYVA 867
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592 AVLCIETSHYVA 603

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RESULT 2

protein F40F12.5 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: F88568
R;anonymous, The C. elegans Sequencing Consortium.
S;Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nemacode C. elegans: a platform for investigating biolog
A;Reference number: A75000, MUID: 99069613; PMID: 9851916
A;Note: see webbilities genome. wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Status: preliminary
A;Notecusion: preliminary
A;Residues: 1-1021 <STO>
A;Cross-references: GB:chr_III; PIDN:CAA82339.1; PID:g3877002; GSPDB:GN00021; CESP:F40F1
A;Gene: F40F12.5
A;Map position: 3

Gaps ; Query Match 1.3%; Score 12; DB 2; Length 1021; Best Local Similarity 100.0%; Pred. No. 0.0023; Matches 12; Conservative 0; Mismatches 0; Indels

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Mon Apr 18 15:46:04 2005

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Gaps

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Length 215;

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A,Residues: 11448 «PAU»
A,Cross-references: UNIPROT:001754; EMBL:AF003130; NID:g2088663; PID:g2088666; PIDN:AAB5
A,Experimental source: strain Bristol N2; clone F55A12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ridlager, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Desinguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunet, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makathors: Kreft, J.; Sinces, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Residues: 1-450 <GLA>
A, Cross-references: UNIPROT: Q8Y4R7; GB: NC_003210; PIDN: CAD00445.1; PID: 916411855; GSPDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucose-6-phosphate isomerase [imported] - Listeria monocytogenes (strain EGD-e)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Date: 20.Sep-1999 #sequence_revision 20-Sep-1999 #text. C,Accession: T15188
C;Accession: T15188
Ballety, A.; Gattung, S.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F55A12.
A;Reference number: 218305
A;Accession: T15188
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 40/1; 98/2; 198/1; 232/1; 251/2; 370/2; 409/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F55A12.6 - Caenorhabditis elegans
                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches
                                                                                                              Query Match 0.8%; Score 8; DB 2
Best Local Similarity 100.0%; Pred. No. 9;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: glucose-6-phosphate isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain EGD-e
                                                                                                                                                                                                                                                                                                                                              138 VELLEEGR 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             540 SLQPVSNQ 547
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                                                                                                                                                                                                                                                                   164 VELLEEGR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLOPVSNQ 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: CESP:F55A12.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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                                           A;Gene: PA3973
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       C, Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable transcription regulator PA3973 [imported] - Pseudomonas aeruginosa (strain PAO1 | Species: Pseudomonas aeruginosa | Species: Canara | Speci
                                                                                                                                                                                                                                                                                       C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S65996; D70086
B;Ogasawara, N.; Nakai, S.; Yoshikawa, H.
B)NA Res. 1, 1-14, 1994
A;Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chrom
A;Reference number: S65967; MUID:96051385; PMID:7584024
A;Accession: S65996
A;Statuus: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-150 cOGA>
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A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16108.1; PID:e1184797
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                   transcription regulator homolog yybA - Bacillus subtilis
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856 AVLCIETSHYVA 867
                                                           886 AVLCIETSHYVA 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 SGFTSEEK 121
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A,Gene: yybA
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Gaps

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Length 448;

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Gaps

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Length 450;

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Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Fitle: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C64765
A;Astatus: nucleic acid sequence not shown; translation not shown
A;Residues: 1-486 <BLAT>
A;Residues: 1-486 <BLAT>
A;Cross-references: UNIPROT:P77199; GB:AE000144; GB:U00096; NID:gl786568; PIDN:AAC73474
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Ohgiya, S.; Goda, T.; Ishizaki, K.; Morimoto, M.; Sakamoto, T.; Kamataki, T.; Shinriki
submitted to JPID, September 1992
A;Reference number: JS0746
A;Accession: JS0746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-524 cOHGS
A; Residues: 1-524 cOHGS
A; Cross-references: DDBJ:D12977; NID:g220307; PIDN:BAA02354.1; PID:g220308
A; Note: this is a revision to the sequence from reference JX0189
A; Note: the source is designated as golden hamster
C; Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C; Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-551 <POH3-
A;Cross-references: UNIPROT:P53730; EMBL:271645; NID:g1302524; PID:g1302525; MIPS:YNR030
A;Experimental source: strain 5288C
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C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: S63361
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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F;461/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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N/Alternate names: hypothetical protein N3265
                                                                                                                                                                                                                                                                                                                                                                     Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                          A, Gene: yair F_11-28/Domain: signal sequence #status predicted <SIG> F_129-486/Product: yair protein #status predicted <MAT>
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100.0%; Pred. No. 20;
iive 0; Mismatches
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A,Map position: 14R
                                                                                                                                                                                                                                                                                                                                                                  0.8%; Score 8; I
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - Chinese hamster
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                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 SDYAGPGD 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 SDYAGPGD 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 TELLLAIT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: JS0746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14
                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                             C;Accession: D88950
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Fitle: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Status: preliminary
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: C64765
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q928R6; GB:AL592022; PIDN:CAC97693.1; PID:g16414988; GSPDB:G
A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:044617; GB:chr_V; PIDN:AAB94210.1; PID:g2736431; GSPDB:GN000
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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100.0%; Pred. No. 17;
ive 0; Mismatches
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.00.0%; Pred. No.
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Best Local Similarity 100
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.8
Best Local Similarity 100.
Matches 8; Conservative
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C, Genetics:

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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: F75530
C;Accession: F75530
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
Science 286, I571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q9RXG0; GB:AE001895; GB:AE000513; NID:g6458024; PIDN:AAF0993
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-1086 <MAG>
A;Residues: 1-1086 <MAG>
A;Cross-references; UNIPROT:Q9TYN3; EMBL:AF125451; PIDN:AAD12824.1; GSPDB:GN00022; CESP:A;Experimental source: strain Bristol N2; clone Y37E11B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Y37E11B.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%; Score 8; DB 2; Length 1086; 100.0%; Pred. No. 38; 0; Indels ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 760;
        0; Indels
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A;Description: The sequence of C. elegans cosmid Y37E11B.
A;Reference number: Z21433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 1
C;Superfamily: virulence-associated protein vacB homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: T33893
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Introns: 77/3; 305/3; 540/2; 729/2; 761/2; 981/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.8%; Score 8; DB 2;
100.0%; Pred. No. 28;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      ribonuclease - Deinococcus radiodurans (strain R1)
        Mismatches
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        8; Conservative
                                                                                         675 PEEFLNIL 682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 NITDLLED 30
                                                                                                                                                                         48 PEEFLNIL 55
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Best Local Similarity
Matches 8; Conserv
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Matches 8; Conserv
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        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable AMP-binding enzyme PA1997 [imported] - Pseudomonas aeruginosa (strain PA01) C.Species: Pseudomonas aeruginosa (C.Species: Pseudomonas aeruginosa (C.Species: Pseudomonas aeruginosa (C.Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 (C.Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 (C.Species: 15-Sep-2004 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 (C.Species: 15-Sep-2004 #sequence_revision #sequence_revisi
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E69420
C) Species expression/formation regulatory protein (hypF) homolog - Archaeoglobus fulgit C) Species: Archaeoglobus fulgidus
C) Species: Archaeoglobus fulgidus
C) Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 14-Apr-2003
C) Accession: E69420
C) Recession (R) A.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson Fiklenk, H.P.; Clayton, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. A.; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A.; Altle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A.; Accession: E69420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q912B2; GB:AE004626; GB:AE004091; NID:g9947995; PIDN:AAG0538
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-740 <KLLS> A;Cross-references: GB:AE001009; GB:AE000782; NID:g2689332; PIDN:AAB89876.1; PID:g264926 C;Superfamily: carbamoyl phosphate-converting enzyme ([NiFe]-hydrogenase maturation fact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A,Reference number: A82950; MUID:20437337; PMID:10984043
A,Accession: G83395
A,Status: preliminary
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100.0%; Pred. No. 24;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length S51
                               F;56-72/Domain: transmembrane #status predicted <TW2>
F;141-157/Domain: transmembrane #status predicted <TW3>
F;165-182/Domain: transmembrane #status predicted <TW4>
F;187-203/Domain: transmembrane #status predicted <TW4>
F;210-226/Domain: transmembrane #status predicted <TW5>
F;308-324/Domain: transmembrane #status predicted <TW5>
F;333-348/Domain: transmembrane #status predicted <TW7>
F;353-379/Domain: transmembrane #status predicted <TW3>
F;3-19/Domain: transmembrane #status predicted <TM1>F;56-72/Domain: transmembrane #status predicted <TM2
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F;135-619/Domain: acetate-CoA ligase homology <ACL>
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100.0%; Pred. No. 21;
tive 0; Mismatches
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A;Residues: 1-651 <STO>
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Sequence 49940, A
Sequence 271965,
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Sequence 489, App
Sequence 290, App
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APPLICANT: INCYTE PERET.
APPLICANT: TANG, Y. Tom
APPLICANT: TANG, Y. Tom
APPLICANT: TANG, Y. Tom
APPLICANT: WILLMAN, Jennifer L.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: GUELEY, Neil C.
APPLICANT: GUELEY, Neil J.
APPLICANT: AZIMZAI, Yalda
APPLICANT: BAUGHN, Mariah R.
TITLE OF INVENTION: HUMAN CYTOSKELETON ASSOCIATED PROTEINS
FILE REFERENCE: PF-0594 PCT
CURRENT APPLICATION NUMBER: US/10/921,707
CURRENT FILING DATE: 2004-08-19
                                                                                                                                                                                                                                                                                                                               0 US-09-908-975-15332

0 US-10-719-993-10379

0 US-10-741-600-27455

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3 US-10-027-632-187795

10S-09-919-9187795

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-MODEL=frame+ p2n.model -DEV=xlp
-O=/cgn2 1/USPTO spool p/USO8671687/runat 15042005 163040 12059/app query.fasta_1.1095
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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PRIOR FILING DATE: 2001-06-25
PRIOR PILING DATE: 2001-06-25
PRIOR PRICATION NUMBER: 09/156,470; unassigned; 60/131,321
PRIOR FILING DATE: 1998-09-18; 1998-09-18; 1999-04-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PERL PROGRAM
SEQ ID NO 25
LENGTH: 4527
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                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID
US-10-921-707-25
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98.44%
98.44%
74.92%
                                           TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No.:
Score:
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Best Local Similarity:
Query Match:
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| IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAgpGlyVa| 179
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Sequence 3, Application US/09851673
Publication No. US20030165985A1
GENERAL INFORMATION:
APPLICANT: Derry, Jonathan
APPLICANT: Panslow, Milliam
APPLICANT: Pougall, William
APPLICANT: Dougall, William
APPLICANT: Dougall, William
APPLICANT: Dougall, William
TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR CD40 &
FILE REFERENCE: 3198
CURRENT APPLICATION NUMBER: US/09/851,673
CURRENT APPLICATION NUMBER: US/09/851,673
SOFTWARE: PatentIn version 3.0
SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 5371
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                                            RESULT 3
US-10-755-889-489
; Sequence 489, Application US/10755889
; Sequence 489, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: BAISED-I-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE JATTLE OF INVENTION: PATHWAY
; FILLE REFERENCE: D0204 NP
; CURRENT APPLICATION NUMBER: US. 60/440,068
; CURRENT FILING DATE: 2004-01.14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; RILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 489
; LINGTH: 5371
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ORGANISM: Homo sapiens
US-10-755-889-489
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Best Local Similarity:
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701 LygValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGluLysValGlyVal 72	Oy 761 LystlePheProSeriedGlubeushliffspleeUslussplintFirstgin 780 1569 AAAATTTTCCTTCTCTGAATTAAATATAACAGATTTACTTGAAGACACTCCCAGACAG 1628 Oy 781 CysArglleCysGlyGlyLabametTyrGluCysArgGluCysTyrAspAspProAsp 800 1629 TGCCGGATATGTGGAGGCCTTGCAATGTATGAGTGTAGAGAATGCTACGACGATCCGGAC 1688 Oy 801 ileSeralaGlyLysglleLysGluPheCysLysThrCysAsaThrGluValHisteuHis 820	Db	861 GluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSerAlaTrpLeuPhe	Qy 901 ProCysProGluValGluTyrLeuLysMetSerLeuGluAspLeuHisSerLeuAsp 920 Db 1989 CCATGCCCAGAAGTAGCAGAGTACTTGAAGATGTCTCTGGAAGACCTGCATTCCTTGGAC 2048 Qy 921 SerArgArg1leGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyrMetCysMetTyr 940 Db 2049 TCCAGGAGAATCCAAGGCTGTGCACGAAGACTGCTTTGTGATGCATATATGTGCATGTAC 2108	Qy 941 GlnSerProThrMetSerLeuTyrLys 949 Db 2109 CAGAGTCCAACAATGAGTTTGTACAAA 2135 RESULT 5 US-10-117-722-290 Sample 90 annlication HS/1011772	GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Liu, Chenghua APPLICANT: Abundi, Vinod APPLICANT: Abundi, Vinod APPLICANT: Drmanac, Radoje T. APPLICANT: Drmanac, Radoje T. APPLICANT: Drmanac, Radoje T. TITLE OF INVENTION: No. US20030219744Alel Nucleic Acids and	; TITLE OF INVENTION: POLYPEDINGS ; TITLE REPERBNCE: 784CTP2BCIP ; CURRENT APPLICATION NUMBER: US/10/117,722 ; CURRENT FILLING DATE: 2002-04-04 ; PRIOR APPLICATION NUMBER: 09/620,312 ; PRIOR FILLING DATE: 2000-07-19 ; PRIOR APPLICATION NUMBER: 09/552,317 ; PRIOR PILLING DATE: 2000-04-25 ; PRIOR PILLING DATE: 2000-01-21
342 AsnArgArgSerGluLeuPheTyrThrLeuAsnGlySerSerValAspSerGlnPro 360	ABNSELLEUTHTTATGLUASNALGPHEHISSELLEUPROPHESELLEUTHLIVSMELPROFILELITTATGLEUTHLIVSMELPROFILELITTATGACCTGACCAGAACGATTCCACTGTTTACCATTCACTGTCTCACCAGAGATGCCCASGACTTCACTGTTCAGTCTCACCAAGATGCCCASGACATTCACTGTTCAGTCTCACCAAGATGCCCASGACTGTTATGACCATGTGGTNSELAGTGCAAGATGGGCCAGTCTCTGTCAGTCCAAGATGGAAAAGAATGGGCCACAGTCCACTGTTCTGTCAGTCCAATGGTAATGGAAAAGAATGGAAATGGAAATGGAAATGGAAATGGAAATGGAAATGGAAATGGAAAAGAATGGTCCACTTTCTGTCAGTCCAATCTGTAATGGAAA	441 GludeudsnThrAlaProValGinGiuSerProProLeudlaNetProProGlyAsnSer 460	ATCGTTGGATCGGTCAGCCACGGGACTGGATGGAGGCTCGCTGGGACTGGGAAAGGGGAAGGAA	849 CTGAAGAAGACGCTGTTTGTGAAGAGCTGCAGGCCTGACTTTGCATCA 908		TICTGCTTATTTGCTTTTAGTTCTGTTCTGGACTGTGTTACTTAGACCCAAAGAAAG	661 Lysvaldialadasaridicitcitcitcitcitcitcitcitcitcitcitcitcit

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Matches:
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Mismatches:
Indels:
Gaps:
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    1.0
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pt_f_genes Version 1.
SEQ ID NO 290
LENGH: 2523
TYPE: DNA
ORGANISM: Homo sapiens
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                                           Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                       FEATURE:

, NAME/KEY: CDS

, LOCATION: (81).

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                                                       GTGGAGGCTGCATCAGGATTTACCTCTGAAGAAAAAGATCCTGAGGAATTCTTGAATATT
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   876 GATGTAGAATATTATAGTGAAACCCAAGAGCTACTGAGGACAGAAATTGTTAATCCTCTG
                                                                                                        ValGluAlaAlaSerGlyPheThrSerGluGluLysAspProGluGluPheLeuAsnIle
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APPLICANT: Batle, Jon H.
APPLICANT: Carroll, Eddie III
APPLICANT: Carroll, Eddie III
APPLICANT: Catino, Theodore J.
APPLICANT: Dwived, Poornima
APPLICANT: Thiagalingam, Arnthathi
APPLICANT: Thiagalingam, Arnthathi
APPLICANT: Lewis, Marcia E.
TITLE OF INVENTION: Expressed in Cancer Tissue
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CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/237,271
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 4494
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4253
LENGTH: 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4253, Application US/09969034; Publication No. US20040110668A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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                                                    SerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyrMetCysMetTyr
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                                                                                                                                                                                                                      Sequence 204, Application US/10264237

| Sequence 204, Application US/10264237
| Publication No. US20040009491A1
| GENERAL INFORMATION:
| APPLICANT: Birse et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
| FILE REFERENCE: PA131P1
| CURRENT APPLICATION NUMBER: US/10/264,237
| CURRENT FILING DATE: 2002-10-04
| PRIOR APPLICATION NUMBER: PCT/US01/16450
| PRIOR APPLICATION NUMBER: PCT/US01/16450
| PRIOR APPLICATION NUMBER: US 60/205,515
| PRIOR PILING DATE: 2000-05-19
| NUMBER OF SEO ID NOS: 2876
| SOFTWARE: Patentin Ver: 3.1
| SEO ID NO 204
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Matches:
Conservative:
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                                                                                                                                                2109 CAGAGTCCAACAATGAGTTTGTACAAA 2135
                                                                                                                        941 GlnSerProThrMetSerLeuTyrLys 949
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NAME/KEY: misc_feature
LOCATION: (15)...(15)
CTHER INFORMATION: n equals a,t,g,
FEATURE:
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,t,g,
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| LOCATION: (1136).
| OTHER INFORMATION: n equals a,
| FEATURE:
| NAME/KEY: misc_feature
| LOCATION: (1142)...(1142)
| OTHER INFORMATION: n equals a,
| US-10-264-237-204
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NAME/KEY: misc feature
LOCATION: (1113). (1113)
CTHER INFORMATION: n equals
FEATURE:
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Best Local Similarity:
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US-10-264-237-204/c
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PAI31P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
FRIOR PEPLICATION NUMBER: PCT/US01/16450
FRIOR FILING DATE: 2001-05-19
FRIOR FILING DATE: 2001-05-19
FRIOR APPLICATION NUMBER: US 60/205,515
FRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOGTWARE: Patentin Ver. 3.1
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Mismatches:
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Matches:
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                                                                         FEATURE:

NAME/KEY: misc feature

LOCATION: (691). (691)

OTHER INFORMATION: n is unknown.
US-10-761-370-3
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165.00
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                    LENGTH: 2116
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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| Sequence 3, Application US/10761370
| Publication No. US20040219615A1
| Sequence 3, Application No. US20040219615A1
| Sublication No. US20040219615A1
| APPLICANT: WOMALENCH, David
| APPLICANT: WOMALENCO, Andrei
| TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TITLE OF INVENTION: MODULACH=27
| CURRENT APPLICATION NUMBER: US/10/761,370
| CURRENT APPLICATION NUMBER: US/09/646,403
| PRIOR FILING DATE: 1990-03-19
| PRIOR PELING DATE: 1990-03-19
| PRIOR PLING DATE: 1999-03-19
| PRIOR FILING DATE: 1999-03-18
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Matches:
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; NAME/KEY: misc_feature
; LOCATION: 517, 586
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-4253
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                                                  uGlulleMetlleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeuAs
491 CACCTGTGCCCTGAAGAARGCGCTGTTTGTGAAACTGAAGAGCTGCAGGCCTGACTCTAG
                                                                                                    YG1yTyrLeuSerG1uVa1Va1G1uG1uAsnThrProProLysMetG1uLysG1uG1yLe
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                                   gPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPheGl
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APPLICANT: Burgess, Christopher C.
APPLICANT: Astle, Jon H.
APPLICANT: Carrol, Eddie III
APPLICANT: Carrol, Theodore J.
APPLICANT: Carrol, Poornima
APPLICANT: Dwived, Poornima
APPLICANT: Dwived, Poornima
APPLICANT: Thiagalingam, Arunthathi
APPLICANT: Thiagalingam, Arunthathi
APPLICANT: Thiagalingam, Arunthathi
APPLICANT: Lewis, Marcia E.
TITLE OF INVENTION: Bexpessed in Cancer Tissue
FILE REFERENCE: 1657/1032
CURRENT APPLICATION NUMBER: 08/09/969,034
CURRENT PILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/237,271
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 4494
SOFTWARE: FastSEQ for Windows Version 4.0
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Mismatches:
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Matches:
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LOCATION: 429, 468, 523
OTHER INFORMATION: n = A,T,C
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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US-09-969-034-4254/c
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Conservative:
Mismatches:
Indels:
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1 LOCATION: (1004)

1 CHER INFORMATION: n equals a,t,g,

US-10-264-237-205
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NAME/KEY: misc_feature
LOCATION: (984)..(984)
OTHER INFORMATION: n equals a,t,g,
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                                                                 NAME/KEY: misc_feature
LOCATION: (5)...(5)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (9)..(9)
OTHER INFORMATION: n equals
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LOCATION: (307)...(307)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (948)...(948)
OTHER INFORMATION: n equals
              TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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Sequence 1386, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
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                                                                                                                                                                                                                                                                                  NN: MAP TO AC007728.1

NN: EXPRESSED IN BT474, SIGNAL = 0.98

NN: EXPRESSED IN PETAL LIVER, SIGNAL = 0.92

NN: EXPRESSED IN HELLO, SIGNAL = 1.5

NN: EXPRESSED IN HELLO, SIGNAL = 1.5

NN: EXPRESSED IN HELA, SIGNAL = 0.89

NN: EXPRESSED IN PEACENTY, SIGNAL = 1

NN: EXPRESSED IN LUNG, SIGNAL = 1

NN: EXPRESSED IN LUNG, SIGNAL = 1.4

NN: EXPRESSED IN BRAIN, SIGNAL = 1.4

NN: EXTRESPEROTHER: Q10427, EVALUE 1.70e-01
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 18145
LENGTH: 309
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR APPLICATION NUMBER: US 09/608,408 PRIOR FILING DATE: 2000-06-30 PRIOR APPLICATION NUMBER: US 09/774,203 PRIOR FILING DATE: 2001-01-29
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ORGANISM: Homo sapiens
FEATURE:
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Sequence 18145, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REPREMENCE: Aeonica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23
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CTTTGCAATGTATGAGTGTAGAGAATGTTACGACCGATCCGGACATCTCAGCTGGAAAAA
                                                                              leLysGlnPheCysLysThrCysAsnThrGlnValHisLeuHisProLysArgLeuAsnH
                                                                                                                              306 rcaagcagririgraaaccrgcaacacrcaagrccaccricarccgaagaggcrgaarc
                                                                                                                                                                                    isLysTyrAsnProValSerLeuProLysAspLeuProAspTrpAspTrpArgHisGlyC
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PRIOR PLILING DATE: 2001-05-23
PRIOR PLILOG DATE: 2000-05-24
PRIOR PPLICATION NUMBER: US 60/180,312
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR PLILOG DATE: 2000-05-26
PRIOR PLILOG DATE: 2000-06-30
PRIOR PLILOG DATE: 2000-08-30
PRIOR PLILOG DATE: 2000-08-30
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PLING DATE: 2001-01-30
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APPLICATION NUMBER: US 6
FILING DATE: 2000-09-21
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US-09-864-761-18145/c
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                                                          LeudanThralaProValGlnGluSerProProLeudlaMetProProGlydsnSerHis
                                                                                                                                                           GlyLeuGluValGlySerLeuAlaGluValLysGluAsnProProPheTyrGlyValIle
                                                                                                                                                                                                            303 GGTCTAGAAGTGGGCTCATTGGCTGAAGTTAAGGAGAACCCTCCTTTCTATGGGGTAATC
                                                                                                                                                                                                                                                            482 Argrrp1leGlyGlnProProGlyLeuAsnGluValLeuAlaGlyLeuGluLeu 499
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; Sequence 35878, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; TITLE OF INVENTION: EROM VARIOUS cDNA LIBRARIES
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FREESEQ for Windows Version 3.0
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Patent No. US20020137160A1
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Wengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
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OTHER INFORMATION: n = A,T,C or
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Best Local Similarity:
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US-09-918-995-35878
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US-09-983-965-1633
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LENGTH: 425
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N: EXPRESED IN FETAL LIVER, SIGNAL = 0.92

N: EXPRESED IN HELLO, SIGNAL = 1.5

N: EXPRESED IN HELA, SIGNAL = 1.3

N: EXPRESED IN PLACENTA, SIGNAL = 1

N: EXPRESED IN HEART, SIGNAL = 0.89

N: EXPRESED IN LUNG, SIGNAL = 0.89

N: EXPRESSED IN LUNG, SIGNAL = 1.3

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.3

N: EXPRESSED IN BRAIN, SIGNAL = 1.3
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILLING DATE: 2000-02-04
PRIOR PILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/23,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILLING DATE: 2000-06-36
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELICATION NUMBER: DCT/USO1/00666
PRIOR PELICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR PELICATION NUMBER: PCT/USO1/00667
PRIOR PELICATION NUMBER: PCT/USO1/00669
PRIOR PELICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PELICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR PELICATION NUMBER: US 09/774,203
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING 
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ORGANISM: Homo sapiens
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Conservative: Mismatches:

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534 ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsn 552
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; Sequence 15332, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
    APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, B1;
    APPLICANT: MINTZ, Liat
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; TILLE REPRENCE: 36680-0005
; CURRENT APPLICATION NUMBER: US 60/221,607
; PRIOR PILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SEQ ID NO 15332
; LENGTH: 60
; LENGTH: 60
; LENGTH: 60
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION FILE OF INVENTION: MUSCLE AND FAT DEPOSITION CENTRAL STATISTICAL (10.27) CURRENT APPLICATION NUMBER: US 09/465,231 PRIOR PILING DATE: 1999-12-15 PRIOR PILING DATE: 1999-12-15 PRIOR FILING DATE: 1999-12-17 SEQ ID NOS: 5912 SEQ ID NOS: 5912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     750 ProArgPheGlyLysAspPheLysLeuPheLysLysIlePheProSerLeuGluLeuAsn 769
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US-09-983-965-1633
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Matches:
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                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: BOS taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
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; ORGANISM: Homo &
US-09-908-975-15332
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Add (0196 Human pol Ab189642 Human pol Ab261081 cDNA enco Ab207515 Human col Ab207515 Human col Ab207515 Human col Ab189643 Human col Ab189643 Human col Ab471948 Human col Ab20692 Probe #10 Aba65741 Human foe Aba47848 Human ben Aba47848 Human ben Aba47848 Human ben Aba47849 Human col Aba47849 Human col Aba47849 Human col Aba42721 Human pen Aba42721 Human ben Aba1393 Probe #13
     Adi98410 Human pol
Add98620 DNA encod
Adb48380 Novel hum
Aas41617 cDNA enco
Aahl8625 Human cDN
Adq95919 T cell ac
Aahl8478 Human cDN
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Aas90524 DNA encod
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Aai01393 Probe #
Abs01449 Human g
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ADQ95919
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ABQ60558
AAZ07515
ABL89643
AAH07749
ABQ60559
ADK71948
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ABA47848
ABA32825
AAK39883
AAK14143
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ADK71946
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                       ADB48380
AAS41617
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AAI32754
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AAK26850
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ABA65741
                                                      AAH18478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      ADQ95917 standard; cDNA; 3302 BP
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WO2004058805-A2
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ADQ95917;
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Adq95917 T cell ac
Adc24898 Human bre
Aaa08599 Human cyt.
Abv75394 Human CYL
Adr14488 Human NF.
                                                              (without alignments)
5221.036 Million cell updates/sec
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                                                                                                   MSSGLWSQEKVTSPYWEERI.....RLLCDAYMCMYQSPTMSLYK 949
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                                                     April 17, 2005, 01:25:02; Search time 1076 Seconds
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       version 5.1.6
- 2005 Compugen Ltd.
                                      nucleic search, using frame_plus_p2n model
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      AAATTTCCTGGAGTTGTACGCTTCAGAGGACCCCTGTTAGCAGAGAGGACAGTCTCCGGA
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                                                                                                                                                                                                                                                                                                               The invention relates to purified proteins and genes encoding them, that are involved in T cell activation (I) and has an amino acid deletion, substitution or addition in the amino acid sequences. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of autoimmune disease (rheumatoid arthritis, asthma, multiple sclerosis and diabetes), allergic disease, infectious disease, AIDS, and acute or chronic rejection at organ transplant or bone marrow transplant. This sequence corresponds to a cDNA for a protein involved in T cell activation.
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                                                                                                                                                                                                          New purified protein involved in T cell activation, useful for diagnosing, preventing and/or treating acquired immunodeficiency syndrome, autoimmune (e.g. rheumatoid arthritis, and diabetes), allergic and infectious diseases.
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26-DEC-2002; 2002JP-00376365.
27-DEC-2002; 2002US-0436473P.
25-APR-2003; 2003US-0455792P.
21-OCT-2003; 2003US-0465792P.
22-OCT-2003; 2003US-0512846P.
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The invention relates to breast specific polypeptides (BSPs) and nucleic acids (Dreast specific nucleic acids, BSNAs) encoding them. The invention acids to vectors and host cells comprising a BSNA sequence; antibodies against BSPs; the recombinant production of BSPs; methods of detection of BSNAs or BSPs in a sample; kits for detecting a risk of cancer for presence of cancer in a patient; and vaccines comprising a BSNA or BSP. The invention additionally discloses fragments, methods for proteins, homologous proteins and allelic variants of BSPs; methods for identifying and designing agoinists and artegonists of BSPs; methods for identifying and monitoring breast itssue; producing engineered breast identifying and monitoring breast; producing engineered breast cissue for treatment and research; producing ransgenic animals and cells comprising BSNA sequences; aptemers evolved to bind spocifically to BSPs; and single exon probes based on BSNA sequences. BSPs and single exon probes based on BSNA sequences. BSNAs and antibodies against BSPs are useful for identifying, diagnosing, and non-cancerous disease states in breast tissue. Sabs and BSNAs may additionally be used to identify and monitor breast tissue, in screening for BSP agonists and antagonists, and in the
                                                                                                                                                                                                      New breast specific polypeptide useful for identifying, diagnosing, monitoring, staging, imaging and treating breast cancer and non-cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  breast cancer; metastasis; non-cancerous disease; breast tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; breast specific polypeptide; BSP; breast specific nucleic acid;
                              2882 IGCCTGGCTCTTCTTTGACAGCATGGCGATGGGGATGGTGGTCAGAATGGCTTCAACAT
                                                                                                                      TCCTCAAGTCACCCCATGCCCAGAAGTAGGAGAGTACTTGAAGATGTCTCTGGAAGACCT
                                                                                                                                                                              uHisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTy
876 rAlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIl
                                                                                        eProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLe
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ction of engineered breast tissue for treatment or research. BSNAs lso be used in gene therapy and in the production of transgenic ls and cells. The present sequence represents a breast specific ic acid (BSNA) used in an example of the invention.	cores: 0 754.00 ilarity: 98.54 Similarity: 98.54 :	687A-3 (1-949) x ADC24898 (1-6831)	1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArglle 20	21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLys 40	45	41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgile 60 	61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80	O 59	81 ValleuPheValAspGluAspValValGluIleAsnGluLysPheThrGluLeuLeu 99 	0	ιO Η	120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139 	0 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 15	5 AAATITICCIGGAGIIGIACGCIICAGAGGACCCCIGTIAGCAGAGGACAGGCICCGGA 20 0 Ilabbabagiwajianianianianianianianianianianianianiani	Incomparing the comparing th	0 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGlyPheValAlaLeuAsp 198	o incendedonantacettiiileneiteneitenitaanitaanitaitaanitaitaanitaitaatiitaan		9 AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLy	ıo	9 -GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSe 258	1 - CONGRESSION OF THE COORDINATION OF THE CONTROL	
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Q	2424	IGGAGTGCACTTTGTAGTTTTGCGTGTGTAAAAGTACAATTCTATTGCACATCAA 24
ò	297	uAlaPheMetSe 31
οg	2484	IATCATCCCAGAGAGTGTGACGCAGGAAAGGAGGCCTCCCCAAACTTGCCTTTATGTC 25
λŏ	317	rArgGlyValGlyAspLySGlySerSerHisAsnLysProLysAlaThrGlySerTh 337
qq	2544	361GTTGGGGACAAAGGTTCATCCATAATAAACCAAAGGCTACAGGATCTAC 26
à	337	rAspProGlyAsnArgArgSerGluLeuPheTyrThrLeuAsnGlySerSerVa 35
QQ	2604	
ò	356	SerGinProGinSerLysSerLysAanThrTrpTyrIleAapGluValAlaGluAs
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ф	2844	CACCAAGATGCCCAATACCAATGGAAGTATTGGCCACAGTCCACTTTCTCTGTCAGCCCA 2903
ò	436	nSerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPr 456
qq	2904	GICTGTAATGGAAGAGCTAAACACTGCACCGTCCAAGAGAGTCCACCTTGGCCATGCC 2963
ò	456	OProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPr 476
qq	2964	TCCTGGGAACTCACATGGTCTAGAAGTGGGCTCATTGGCTGAAGTTAAGGAGAACCCTCC 3023
ò	476	oPheTyrGlyVallleArgTrplleGlyGlnProProGlyLeuAsnGluValLeuAlaGl 496
qq	3024	TITCTATGGGGTAATCCGTTGGATCGGTCAGCCCCCAGGACTGAATGAA
δλ	496	VLeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTy 516
qq	3084	
ò	516	rPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSe 536
qq	3144	-C)
ò	536	JPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPh 5
Ор	3204	JITTGCATCATTGCAGCCGGTTTCCAATCAGATTGAGCGCTGTAACTCTTTAGCATT 3
ò	556	GlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGl 5
Ор		TGGAGGCTACTTAAGTGAAGTAGTAGAAAATACTCCACCAAAAATGGAAAAAAGAAGG 3323
ò	576	3lnGlyHisTyrAsnSerCysTyrLe 5
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ò	596	SerValLeuAspThrValLeuLeuAr 6
QQ		aaccitaitcigcitaitigcititagitcigitcigacacigigitacitag 34
ò	616	gProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGl 636
qq	3444	CCCAAAGAAAGAACGATGTAGAATATTATAGTGAAACCCAAGAGCTACTGAGGACAGA 35
δ	636	

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Cytoskeleton associated protein; CYSKP-9; cancer; proliferative; autoimmunity; inflammatory, vesicle trafficking; neurological; cardiovascular; cell motility; reproductive; muscle disorder; ss
                                                                                                                                                                                                                                                          Bandman O,
Baughn MR;
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Azimzai Y,
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Best Local Similarity:
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Guegler KJ,
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proliferative,

to treat cell present neurological,

Corley NC;

AAA08581-96 encode human cytoskeleton associated proteins 1 to 16 (CYSKP-11 to CYSKP-16) respectively. The sequences can be used to treat and diagnose cancer and cell proliferative, autoimmune/inflammatory, vesicle trafficking, neurological, cardiovascular, cell motility, reproductive and muscle disorders. Pharmaceutical compositions containing CYSKP-2 to CYSKP-16 can be used to treat or prevent disorders associated with decreased expression or activity of CYSKP (claimed), for example, attherosclerosis, cirribasis, hepatitis, myelofibrosis, psoriasis, cancers, autoimmune/antinflammatory disorders such as allergies, anemia, asthma, acquired immunodeficiency syndrome (AIDS), Crohn's disease, diabetes mellitus, Goodpasture's syndrome, osteoarthritis, scleroderma and trauma. CYSKP antagonists can be used to treat or prevent a disorder associated GCCTTATGGAGCCAAGAAAAGTCACTTCACCCTACTGGGAAGAGCGGATTTTTTACTTG 329 GGAAGTATAGGACAGTATATTCAAGATCGTTCTGTGGGGCATTCAAGGATTCCTTCTGCA 448 cricitcaagaargcagcgrracagacaaacaaacacaaagcrccrraaagraccga- 388 LeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLysValProLys 43 63 64 LysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAlaValLeuPhe 83 Glyser1leGlyGlnTyr1leGlnAspArgSerValGlyHisSerArg1leProSerAla GlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIlePheTyrLeu Sequence 4527 BP; 1351 A; 823 C; 1005 G; 1348 T; 0 U; 0 Other; with increased expression or activity of CYSKP (claimed) 4527 944 0 2 15 Length:
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                                                                                                                                                                                                                                                811eGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSerAlaTrpLe
                                                                                                                                                                                                                                                                         CATAGAAACAAGCCACTATGTTTTTGTGAAGTATGGGAAGGACGATTTTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                            CACCCCATGCCCAGAAGTAGGAGAACTTGAAGATGTCTCTGGAAGACCTGCATTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyrMetCysMe
                 OASDIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGlnValHisLe
                                                                                                                                 2728 TCATCCGAAGAGGCTGAATCATAAATATAACCCAGTGTCACTTCCCAAAGACTTACCCGA
                                                                                                                                                                  PTrpAspTrpArgHisGlyCys1leProCysGlnAsnMetGluLeuPheAlaValLeuCy
                                                                                                                                                                                                                                                                                                                             uPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIleProGlnVa
                                                                                                                                                                                                                                                                                                                                                                   CTTCTTTGACAGCATGGCCGATCGGGATGGTCGAGAATGGCTTCAACATTCCTCAAGT
                                                       GGACATCTCAGCTGGAAAATCAAGCAGTTTTGTAAAACCTGCAACACTCCAAGTCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                       InhrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeuHisSerLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying compounds that alter one or more biological activities of CD40 by modulating the binding of NEMO and CYLD, useful for treating disorders of the immune system, and inflammatory and cancer diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD40; NF-kappaB essential modulator; NEMO; CYLD; immunosuppressive; antiinflammatory; cytostatic; gene therapy; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tTyrGlnSerProThrMetSerLeuTyrLyg 949
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392. .3262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "CYLD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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P-PSDB; ABB82783.
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	1111 TGGAGAACAATAGAATCTGGAACAGTTATATTCTGTGATGTTTTGCCAGGAAAGAAA	3	
2 -	8 rLeuGlyTyrPheValGlyValAspMetAspAsnProlleGlyAsnTrpAspGlyArgPh 2	, XO QQ	613 LLeuLeuArgProLysGluLysAsnAspValGluTyrTyrSerGluThrGluLeuLe 633
27,	eAspGjyvalLeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAs TGAIGAGGAGCTAGAGATTTTGGGGGATTGAGAGAAGAAAGAAA	ζς qq	633 UARGThrGluilevalAsnProbeuArgileTyrGlyTyrvalCysAlaThrLysileMe 653
2 5	nAspilelleProGluSerValThrGlnGluArgArgProProLysLeuAl	λ α	653 tLysleuarglysileleuglulysvalglualaalaserglyphethrserglugluly 673
3 6 113	4 aPheMetSerArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaTh	Qy Dp	673 saspprogluglupheLeuasnIleLeupheHisHisIleLeuargValGluProLeuLe 693
61 6	34 rGlySerThrSerAspProGlyAsnArgArgSerGluLeuPheTyrThrLeuAsnGl 	λ ₀ α	693 uLysileArgSerAlaGlyGlnLysValGlnAspCysfyrPheTyrGlnIlePheMetGl 713
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ı `` <del>-</del>	AlagluAspFroAlaLysSerLeuThrGluIISSerThrAspPheAspArgSerSerPro	. da	733 nSerAsnLeuLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGl 753
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4 -	OCHESETLEUTHILLYSMELFORSTTARGISSCENCISCORGAGAGASAILCCACICI OPheSetLeuThillysMetProAsnThrAsnGlySerIleGlyHisSerProLeu ATTICLEUTHILLIHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ζς qa	773 ubeugluaspThrProArgGInCysArgIleCysGlyGlyLeuAlaMetTyrGluCysAr 793 
i '	33 uSerAlaGlmSerValMetGluGluLeuAsmThrAlaProValGlmGluSerProProLe	ζς qa	793 gGlucysTyrAspAspEroAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCy 813 
4 5	Stractory of the response interference of the strategy of the	ço da	813 SABNThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLe 833 
, , ,	uAsnProProPheTyrGlyVall1eArgTrpIleGlyGlnProProGlyLeuAsnGluVa	& da	833 uProlygaspleuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGl 853
i ` =	3 lleubladlyteudlubeudlubspdlucyshladlycysthraspdlythrPhe	ζ. O	853 uLeuPheAlaValLeuCygileGluThrSerHisTyrValAlaPheValLysTyrGlyLy 873 
-	3 YThrargTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysAr	& a	873 SASPASPSETALATTPLEUPhePheAspSeTMetAlaAspArgAspG1yG1yG1nAsnG1 893
i - 6	33 gProAspSerArgPheAlaSerLeuGlnProValSerAsmGlnIleGluArgCys	ζο da	893 yPheAsnIleProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLe 913 
i - c	3 rLeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGl	<i>₹</i> 0	913 uGludapLeuHisSerLeudspSerArgargIleGlnGlyCysAlaArgArgLeuLeuCy 933 
ν	Insect	ζό Q1	933 SASDAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949 
1 ",	3 rCysTyrLeukspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuksp [	RESUL ADR14-	RESULT 5 ADR14488 ID ADR14488 standard; DNA; 5371 BP.

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Human NF-kappaB pathway-associated gene SeqID489.
 Claim 1; SEQ ID NO 489; 237pp; English.
 Nadler SG, Neubauer MG, Feder JN,
 HIV propagation; gene; ds; human
 BRIM) BRISTOL-MYERS SQUIBB CO
 13-JAN-2004; 2004WO-US000798.
 14-JAN-2003; 2003US-0440068P
 12-MAY-2003; 2003US-0469757P
 (first entry)
 WPI; 2004-562168/54.
P-PSDB; ADR14489.
 WO2004065577-A2
 21-OCT-2004
 05-AUG-2004
 ADR14488;
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subject to the novel association with the NF-kappaB pathway of the Length: was obtained by the indexer from Genbank. Gaps: US-09-671-687A-3 (1-949) x ADR14488 (1-5371) invention. Note: This sequence does 0 685.00 97.63% 97.63% Percent Similarity: Best Local Similarity: gnment Scores: 872 219 1052 392 21 452 41 512 572 81 632 100 692 752 812 160 932 199 992 61 120 140 180 239 Query Match: No.: Score: 888888 ద DP 8 ò 음 ò 셤 ò g 8 셤 ò g ò 셤 ò 셤 à a ò ò 유 8 쉽 ò 셤 This invention relates to the novel association of protein sequences (and the genes which encode them) to the NF-kappaB pathway. The invention may be useful for the production of compounds with an antiniflammatory, cytostatic, hepatotropic, virucide, antiarteriosclerotic, antinheumatic, cytostatic, hepatotropic, virucide, antiarteriosclerotic, manarecry, cytostatic, certainal-den, antiasthmatic, antiarteriosclerotic, manarecry, communomodulator, cerebroprotective, vasotropic, immunosuppressive or unherary activity or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NF-kappaB pathway. The condition is an immune disorder an inflammatory disorder, an inflammatory disorder. an inflammatory disorder claracted to aberrant NF-kappaB regulation, cancer, aberrant apoptosis, related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis, syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HITV-1, cetodermal dysplasia, immunodeficiency, viral infections, HIV-1, HITV-1, cetodermal dysplasia, immunodeficiency, viral replication, host cell survival evasion of immune responses, rheumatoid arthritis, inflammatory by proteomer, stroke, BAB, autoimmune disorders related to aberrant acute phase responses, hypercongenital conditions, birth defects, necrotic lesions, wounds, cogan transplant rejection, conditions related to organ transplant crejection, conditions related to organ transplant crejection, conditions related to organ transplant crejection, concers and HIV propagation in cells infected with other viruses. The present sequence is that of a human gene which is NP-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide; antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic; antiarthratic; antiarthratic; antiarthratic; antiarthratic; contractions of the memomodulator; creebroprotective; vasotropic; immunosuppressive; vulnerary; gene therapy; immune disorder; inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis; hyperig disorder; NF-kappaB regulation; cancer; aberrant apoptosis; hyperig disorder; NF-kappaB regulation; cancer; aberrant apoptosis; viral hyporidrome; hypohidrotic ectodermal dysplasia; immunodeficiency; viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza; viral replication; host call survival; evasion of immune response; rheumatord arthritis; inflammatory bowel disease; colitis; asthma; attendematoric character; hyper immune activity; aberrant acute phase response, hypercongenital condition; birth defect, necrotic lesion; wound; organ transplant rejection; aberrant signal transduction; proliferating disorder; cancer; New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway. Carman J;

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 AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly 238
 rLeuGlyTyrPheValGlyValAspMetAspAsnProlleGlyAsnTrpAspGlyArgPh 278
 511
 751
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 278 eAspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAs 297
 ATGAGTTCAGGCTTATGGAGCCAAGAAAAGTCACTTCACCCTACTGGGAAGAGGGTT 451
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not appear in the specification but
 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle
 -GlyGluThrileGluSerGlyThrValilePheCysAspValLeuProGlyLysGluSe
 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgile
 TTTTACTTGCTTCTTCAAGAATGCAGGGTTACAGACAAAACACAAAAGCTCCTTAAA
 GTACCGAAGGGAAGTATAGGACAGTATATTCAAGATCGTTCTGTGGGGCATTCAAGGATT
 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla
 GTTCTCTTTGTTGAAAGGATGTTGTAGAGATAAATGAAAAGTTCACAGAGTTACTT
 TTGGCAATTACCAATTGTGAGGAGGGTTCAGCCTGTTTAAAAAACAGAAAAGGACTAAGT
 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu
 AAAGGCCTCCAAATAGACGTGGGCTGTCCTGTGAAAGTACAGCTGAGATCTGGGGAAGAA
 11ePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal
 ATATTCTTTGGAGTTGAATTGCTGGAAGAAGGTCGTGGTCAAGGTTTCACTGACGGGGTG
 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp
 GACACAATGCAGGTCGAACTTCCTTCCTTTGGAAATAAACTCCAGAGTTTCTTTGAA-GGT
 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLys
 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu
 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer
 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly
 LysLeuGluLeuIleGluAspAspAspThrAlaLeuGluSerAspTyrAlaGlvProGlv
 T; 0 U; 0 Other;
 Matches:
Conservative:
Mismatches:
Indels:
 Sequence 5371 BP; 1600 A; 950 C; 1183 G; 1638
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297 n     1291	naspileileProGluSerValThrGlnGluargargProProLysLeual 314 	. a	
314 8 1351 C	aPheMetSerArgGlyValGlyAspLysGlySerSerSerSerHisAsmLysProLysAlath 334 	රු සි	673 8AspProGluGluPheLeuAsnIleLeuPheHisHisIleLeuArgValGluProLeuLe 693 
334		& A	693 uLysileArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGl 713 
		& a	713 uLybaanGluLybyalGlyvalProThrIleGlnGlnLeuLeuGluTrpSerPheIleas 733 
373		& A	733 nSerAsnLeuLy8PheAlaGluAlaProSerCy8LeuIleIleGlnMetProArgPheGl 753
393	OProLeuGlnProProProValAsmSerLeuThrThrGluAsnArgPheHisSerLeuPr 	& &	753 yLysaspPheLysLeuPheLysLysllePheProSerLeuGluLeuAsnIleThraspLe 773
413	OPheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLe	<i>ò</i> 8	773 uLeuGluhapThrProArgGlnCyaArgIleCysGlyGlyLeuAlaMetTyrGluCysAr 793 
433	uSerAlaGlaSerValMetGluGluLeuAsnThrAlaProVaGluGlaGluSerProProLe 	<i>ò</i> 8	793 gGlucysfyraspaspProasplleSerAlaGlyLysileLysGlnPhecysLysThrCy 813 
453	uAlaMetProFroGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGl 	<i>8</i>	813 8A8nThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLe 833 
473		<i>े</i> ह	833 UProlygaspleuProaspTrpaspTrpargHisGlyCys1leProcysGlnasnMetGl 853 
493		<i>&amp;</i> ₽	853 uLeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLy 873 
513		<i>&amp;</i> 8	873 8AspAspSerAlaTrpLeuDhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGl 893 
533		<i>è</i> 8	893 yPheAsnlleProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLe 913
553		λ _O	913 uGluAspLeuHisSerLeuAspSerArgArgTleGlnGlyCysAlaArgArgLeuCy 933
573	ULYSG1uG1yLeuG1uI1eMet11eG1yLysLysLysLysG1yIeG1uG1yHisTyrAsnSe 	& 8	933 8A8PAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyrLy8 949 
593	rCysTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrVa 	RESULT ADQ955 ID A	JT 6 5915 ADQ95915 standard; cDNA; 3302 BP.
613	LeukeuargProLysGluLysasnaspValGluTyrTyrSerGluThrGlnGluLeuLe 633 	A X E X	ADQ95915; 07-OCT-2004 (first entry)
633	uArgThrGluIleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMe 653 	XX E	T cell activation associated cDNA #47. ss; gene; antiallergic; antiarthritic; antiasthmatic; antidiabetic;

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 The invention relates to purified proteins and genes encoding them, that are involved in T cell activation (I) and has an amino acid deletion, substitution or addition in the amino acid sequences. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of autoimmune disease (rheumatoid arthritis, asthma, multiple sclerosis and diabetes), allergic disease, infectious disease, AlDS, and acute or chronic rejection at organ transplant or bone involved in T cell activation.
 302
anti-HIV; antimicrobial; antirheumatic; immunosuppressive; neuroprotective; gene therapy; T cell activation; diagnosis; autoimmune disease; rheumatoid arthritis; asthma; multiple sclerosis; diabetes; allergic disease; infectious disease; AIDS; chronic rejection; organ; bone-marrow transplant.
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 allergic
 ATGAGTTCAGGCTTATGGAGCCAAGAAAAGTCACTTCACCTACTGGGAAGAGCGGATT
 nGluLysValThrSerProTyrTrpGluGluArgile
 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys
 New purified protein involved in T cell activation, useful for diagnosing, preventing and/or treating acquired immunodeficiency syndrome, autoimmune (e.g. rheumatoid arthritis, and diabetes), a
 U; 0 Other;
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947
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
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 Gaps:
 (1-3302)
 Claim 4; SEQ ID NO 93; 2828pp; English
 Location/Qualifiers
243. .3104
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 MetSerSerGlyLeuTrpSerGl
 CORP
 26-DEC-2002; 2002JP-00376365.
27-DEC-2002; 2002US-0436473P.
25-APR-2003; 2003JP-00122113.
28-APR-2003; 2003US-0465792P.
21-CT-2003; 2003US-0465592.
22-OCT-2003; 2003US-0512846P.
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 BP; 981 A; 648
 2003WO-JP016715
 (ASAH-) ASAHI KASEI PHARMA
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98.34%
98.34%
 and infectious diseases
 2004-593134/57.
 US-09-671-687A-3 (1-949)
 Yoneta
 Similarity:
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 P-PSDB; ADQ95916.
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 Sequence 3302
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1141 1201 1441 1021 1081 1381 1501 1321 297 482 119 602 139 662 159 722 179 782 198 842 218 902 238 258 337 376 396 416 542 961 436 AAGAGGTGTTGGGGACAAAGGTTCATCCAGTCATAAAAAACCAAAGGCTACAGGATCTAC LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu ATATICITIGEAGITGAATIGCIGGAAGAAGGICGIGGICAAGGITICACIGACGGGGIG TyrglnGlyLysglnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp AAGCTAGAACTCATAGAAGATGATGACACTGCATTGGAAAGTGATTACGCAGGTCCTGGG 1082 TGATGGAGTGCAGCTTTGTAGTTTTGCGTGTGTTGAAAGTACAATTCTATTGCACATCAA rArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerTh cccrecaaaarcrcrracagararcracagacrrrgaccgrrcrcaccaccacca GTTCTCTTTGTTGATGAAAGGATGTTGTAGAGATAAATGAAAAGTTCACAGAGTTACTT TTGGCAATTACCAATTGTGAGGAGAGGTTCAGCCTGTTTAAAAACAGAAACAGACTAAGT AspThrMetGlnValGluLeuProProLeuGluI]eAsnSerArgValSerLeuLysGly rLeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPh eAspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAs CTCAGACCCTGGAAATAGAAACAGATCTGAATTATTTTATACCTTAAATGGGTCTTCTGT 356 lAspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAs TGACTCACAACCACAATCCAAATCAAAAATACATGGTACATTGAAGAAGTTGCAGAAGA nProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLe 1442 GCCTCCTCCTGTGAACTCACTGACCACCGAGAACAGATTCCACTCTTTACCATTCAGTCT ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla ValleuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly AAATTTCCTGGAGTTGTACGCTTCAGAGGACCCCTGTTAGCAGAGAAGGACAGTCTCCGGA IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal GACACAATGCAGGTCGAACTTCCTCTTTGGAAATAAACTCCAGAGTTTCTTTGAA-GGT -GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSe nAspileIleProGluSerValThrGlnGluArgArgProProLysLeuAlaPheMetSe rSerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVa LysLeuGluLeuIleGluAspAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly pProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGl uThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGl 1142 1262 416 1022 278 297 317 1202 337 1322 376 1382 396 423 81 483 100 543 120 603 140 663 160 723 180 783 199 843 219 903 239 258 셤 요 ò

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ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle

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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
 Ren F, Wang D;
Zhang J, Zhao (
 2641 ACGACCGACCIGCACACTCCAGCTGGAAAATCAAGCAGTTTTGTAAAACCTGCAACACTC
 2581 ACACTCCCAGACAGTGCCGGATATGTGGAGGCCTTGCAATGTATGAGTGTAGAAATGCT
 ACTIACCCGACTGGGACTGGAGACACGGCTGCATCCCTTGCCAGAATATGGAGTTATTTG
 leProGlnValThrProCysProGluValGlyGluTyrLeuLygMetSerLeuGluAspL
 3001 TGCATTCCTTGGACTCCAGGAGAATCCAAGGCTGTGCACGAAGACTGCTTGTGATGCAT
 TTCCTCAAGTCACCCCATGCCCAGAAGTAGGAGAGTACTTGAAAGATGTCTCTGGAAAGACC
 euHisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaT
 yrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrG
 | InValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysA
 laValleuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspS
 CTGTTCTCTGCATAGAAACAAGCCACTATGTTTTTGTGAAGTATGGGAAGGACGATT
 erAlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnI
 CTGCCTGGCTCTTCTTTGACAGCATGGCCGATCGGGATGGTGGTCAGAATGGCTTCAAACA
 spleuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheA
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 ATATGTGCATGTACCAGAGTCCAACAATGAGTTTGTACAAA
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 Human polynucleotide SEQ ID NO
 23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-0053450.
14-SEP-2000; 2000US-00653450.
14-SEP-2000; 2000US-00663191.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00693036.
 CDNA; 2523
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 26-DEC-2000; 2000WO-US034263
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 (HYSE-) HYSEO INC
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 ulleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuAr
 GTCTGTAATGGAAGAGCTAAACACTGCACCCGTCCAAGAGAGTCCACCCTTGGCCATGCC
 OProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPr
 rPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSe
 rArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPh
 TGGAGGCTACTTAAGTGAAGTAGTAGAAGAAAATACTCCCACCAAAAATGGAAAAAGG
 YLEUGlu1leMet11eGlyLysLysCly1leGlnGlyHisTyrAsnSerCysTyrLe
 CTTGGAGATAATGATTGGGAAGAAGAAGGCATCCAGGGTCATTACAATTCTTGTTACTT
 AGACTCAACCTTATTCTGCTTATTTGCTTTTTAGTTCTGTTCTGGACACTGTGTTACTTAG
 AATTGTTAATCCTCTGAGAATATATGGATATGTGTGCGCCACAAAAATTATGAAACTGAA
 -GAAAATACTTGAAAAGGTGGAGGCTGCATCAGGATTTACCTCTGAAGAAAAACTCCTG
 rgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGln1lePheMetGluLysAsnG
 GATCAGCAGCTCAAAAGGTACAAGATTGTTATTTATGGAAAAATG
 luLysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnL
 AGAAAGTTGGCGTTCCCACAATTCAGCAGTTGTTAGAATGGTCTTTTATCAACAGTAACC
 heLysLysLysLysllePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluA
 SpThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysT
 nSerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPr
 OPheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGl
 yLeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTy
 ACTGGAACTGGAAGATGAGTGTGCAGGCTGTACGGATGGAACCTTCAGAGGCACTCGGTA
 TTTCACCTGTGCCCTGAAGAGGCGCTGTTTGTGAAACTGAAGAGCTGCAGGCCTGACTC
 TAGGTTTGCATCATTGCAGCCGGTTTCCAATCAGATTGAGCGCTGTAACTCTTTAGCATT
 eGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGl
 uAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuAr
 gProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGl
 g-LysileLeuGluLysValGluAlaAlaSerGlyPheThrSerGluGluLysAspProG
 euLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspP
 TTAAACTATTTAAAAAATTTTTCCTTCTGGAATTAAATATAACAGATTTACTTGAAG
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous size as peripheral nervous size as peripheral nervous size as peripheral nervous and the peripheral nervous as peripheral nervous and the peripheral nervous as the contained of localised neuropathies and central nervous system diseases, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, architicis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
 Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
 Claim 1; SEQ ID NO 613; 10078pp; English.
Drmanac RT;
Goodrich R,
 WPI; 2001-442253/47.
P-PSDB; AAM39254.
Zhou P,
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Sequence 2523 BP; 757 A; 503 C; 557 G; 706 T; 0 U; 0 Other;

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Alignment S Pred. No.: Score: Percent Sim Best Local Query Match DB:	t Scores. : Similarity: al Similarity: tch:	0 641.00 99.55\$ 67.54\$ 4	Length: Matches: Conservative: Mismatches: Indels: Gaps:	2523 668 0 0 3 3	
US-09-671-6	-687A-3 (1-949)	x AAI58410 (1	-2523)		
70	282 LeuCysSer	PheAlaCysValG	uSerThrileLeuLeuH	isileAsnAspileilePro	301
Db 1	129 CTTTGTAGT	TTTGCGTGTGTTGAA	AGTACAATTCTATTGC	CTTTGTAGTTTTGCGTGTGTTGAAGTACAATTCTATTGCACATCAATGATATCATCCCA 18	188
°	302 GluSerVal	ThrGlnGluArgArg	GluSerValThrGlnGluArgArgProProLysLeuAlaPheMetSerArgGl	YValG1Y	321
Db 1	189 GAGAGTGTG	ACGCAGGAAAGGAGG	CCTCCCAAACTTGCCT	GAGAGTGTGACGCAGGAAAGGAGCCTCCCAAACTTGCCTTTATGTCAAAAGGGGTGTTGGG 24	248
,, ,,	322 AspLysGly	SerSerSerHisAsn	LysProLysAlaThrC	AspLysGlySerSerHisAsnLysProLysAlaThrGlySerThrSerAspProGly 34	341
Db 3	249 GACAAAGGT	TCATCCAGTCATAAT	AAACCAAAGGCTACAG	CAAAGGITCAICCAGICAIAAIAAACCAAAGGCIACAGGAICIACCICAGACCCIGGA 30	308
3	342 AsnArg	ArgSerGluLeuPheT	yrThrLeuA	snGlySerSerValAspSerGlnPro 36	360
Dp 3	309 AATAGAAAC	AGATCTGAATTATTT	TATACCTTAAATGGGT	AATAGAAACAGATCTGAATTTTTTATACCTTAAATGGGTCTTCTGTTGACTCACAACCA 36	368
3	361 GlnSerLys	sSerLysAsnThrTrp	TyrlleAspGluValA	eAspGluValAlaGluAspProAlaLysSer 38	80
Db da	369 CAATCCAAA	TCAAAAATACATGG	TACATTGATGAAGTTG	CAATCCAAATCAAAAATACATGGTACATTGATGAAGTTGCAGAAGACCCTGCAAAATCT 42	428
3	381 LeuThrGlu	ulleSerThrAspPheA	BpArgSerS	erProProLeuGlnProProProVal 40	400
Db 4	429 CTTACAGAGATAT	ATATCTACAGACTTTGACCGTT		CTTCACCACCACTCCAGCCTCCTCTGTG 48	488
Oy 4	401 AsnSerLeu	ThrThrGluAsnArg	PheHisSerLeuProF	AsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeuThrLysMetPro 42	420
Db 4	489 AACTCACTG	ACCACCGAGAACAGA	TTCCACTCTTTACCAT	AACTCACTGACCACCAGAGAACAGATTCCACTTTACCATTCAGTCTCACCAAGATGCCC 54	548
O,	421 AsnThrAsn	GlySerIleGlyHis	SerProLeuSerLeus	ABDThrABDGlySerIleGlyHisSerProLeuSerLeuSerAlaGlnSerValMetGlu 44	440
Dp qu	549 AATACCAAT	GGAAGTATTGGCCAC	AGTCCACTTTCTCTG1	ATACCAATGGAAGTATTGGCCACAGTCCACTTTCTCTGTCAGCCCAGTCTGTAATGGAA 60	809
φ,	441 GluLeuAsn	snThrAlaProValGln	nGluSerProProLeu	laMetProProGlyAsnSer 46	09
Dp qu	609 GAGCTAAAC	ACTGCACCCGTCCAA	GAGAGTCCACCCTTGC	GAGCTAAACACTGCACCCGTCCAAGAGAGTCCACCCTTGGCCATGCCTCCTGGGAACTCA 66	668

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sequence represents a human
 and polynucleotides are useful for the treatment of diseases of ophthalmic, neurological, immunological and nephritic systems. They may also be used to treat hormonal dysfunction, cancer, atherosclerosis and diabetes. The antibodies are useful for detecting or quantitating the polypeptide in tissue. The polypeptides can also be used as molecular weight markers and as a food supplement. This sequence represents a humpolynucleotide of the invention.
 GAGAGTGTGACGCAGGAAGGAGGCCTCCCAAACTTGCCTTTATGTCAAGAGGGGTTGGG
 CTTACAGAGATATCTACAGACTTTGACCGTTCTTCACCACCACTCCAGCCTCCTGTG
 AsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGlnSerValMetGlu
 IleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGlyLeuGluLeuGlu
 LeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPheGlyGlyTyrLeu
 LeuCysSerPheAlaCysValGluSerThr1leLeuLeuHis1leAsnAsp1le1lePro
 Asnarg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerValAspSerGlnPro
 AATAGAAACAGATCTGAATTATTATTACCTTAAATGGGTCTTCTGTTGACTCACAACCA
 GlnSerLysSerLysBanThrTrpTyrIleAspGluValAlaGluAspBroAlaLysSer
 AsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeuThrLysMetPro
 AATACCAATGGGAAGTATTGGCCACAGTCCACTTTCTCTGTCAGCCCAGTCTGTAATGGAA
 CATGGTCTAGAAGTGGGCTCATTGGCTGAAGTTAAGGAGAACCCTCCTTTCTATGGGGTA
 AspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyrPheThrCysAla
 GATGAGTGTGCAGGCTGTACGGATGGAACCTTCAGAGGCACTCGGTATTTCACCTGTGCC
 LeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSerArgPheAlaSer
 GluSerValThrGlnGluArgArgProProLygLeuAlaPheMetSerArgGlyValGly
 CAATCCAAATCAAAAAAAAAAAAAGAACATGATGAAGTTGCAGAAAGACCCTGCAAAATCT
 GluLeuAsnThrAlaProValGluGluSerProProLeuAlaMetProProGlyAsnSer
 GAGCTAAAACACGCGCCCCGTCCAAGAGAGTCCACCTTGGCCATGCCTCCTGGGAACTCA
 HisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProProPheTyrGlyVal
 ATCCGTTGGATCGGTCAGCCCACCAGGACTGAATGAAGTGCTCGCTGGACTGGAACTGGAA
 creaagaagececretricreaaacreaagecrecagecreacreragerrrecarea
 AspLysGlySerSerHisAsnLysProLysAlaThrGlySerThrSerAspProGly
 LeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGlnProProProVal
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Mismatches:
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 Sequence 2523
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 The invention describes an isolated polynucleotide (I) comprising a fully defined (S1) of 749, 3188, 2484, 1169, 2936, 1467, 5773, 5714, 4041, 1372, 3996, 3945, 2735, 1788, 585, 1782, 927, 5714 or 2282 nucleotides as given in the specification, its translated or protein coding portion, its extracellular portion or its active domain. The GPCR-like polypeptides
 860
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 New G-protein-coupled receptor-like polypeptides and polynucleotides, useful for treating diseases of ophthalmic, neurological, immunological and nephritic systems and hormonal dysfunction, cancer, atherosclerosis and diabetes.
 CCGAAGAGGCTGAATCATAAATATAACCCAGTGTCACTTCCCAAAGACTTACCCGACTGG
 AspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAlaValLeuCysIle
 GAAACAAGCCACTATGTTGCTTTTGTGAAGTATGGGAAGGACGATTCTGCCTGGCTCTTC
 ProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeuHisSerLeuAsp
 ProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAspLeuProAspTrp
 GACTGGAGACACGCCTGCCTTGCCAGAATATGGAGTTATTTGCTGTTCTCTGCATA
 .uThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSerAlaTrpLeuPhe
 eProGlnValThr
 TTTGACAGCCATGGCCGATCGGGATGGTCGTCAGAATGGCTTCAACATTCCTCAAGTCACC
 CCATGCCCAGAAGTAGGAGAACTTGAAGATGTCTCTGGAAGACCTGCATTCCTTGGAC
 antiatherosclerotic;
 ophthalmological; immunomodulatory; cytostatic; antiatherosclerotic
antidiabetic; GPCR-like protein; ophthalmic disorder;
neurological disorder; immunological disorder; nephritic disorder;
hormonal dysfunction; cancer; atherosclerosis; diabetes;
molecular weight marker; food supplement; human; ss.
 PheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIl
 DNA encoding human GPCR-like protein segid 290.
 2; SEQ ID NO 290; 92pp; English
 GlnSerProThrMetSerLeuTyrLys
 BP.
 ADQ98620 standard; cDNA; 2523
 RT
 2000US-00488725
2000US-00552317
 19-JUL-2000; 2000US-00620312
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 (HYSE-) HYSEQ INC
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1989 CCATGCCCAGAAGTAGGAGAGTACTTGAAGATGTCTCTGGAAGACCTGCATTCCTTGGAC 2048
 940
 The invention relates to a polynucleotide comprising a sequence given in the specification, or its mature protein-cading portion, or its scomplement. The polynucleotide is useful for treating diseases e.g., cancer or neurodegenerative diseases and many others listed in the specification. The present sequence represents a novel human cDNA. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030104529.
 SerArgArg11eG1nG1yCysAlaArgArgLeuLeuCysAspAlaTyrMetCysMetTyr
 2049 TCCAGGAGAATCCAAGGCTGTGCACGAAGACTGCTTTGTGATGCATATATGTGCATGTAC
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 e.g., cancer
 Sequence 2523 BP; 757 A; 503 C; 557 G; 706 T; 0 U; 0 Other;
 2523
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 diseases
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 Drmanac
 ss; cancer; neurodegenerative disease; human.
 2135
 949
 treating
 US-09-671-687A-3 (1-949) x ADB48380 (1-2523)
 Claim 1; SEQ ID NO 290; 99pp; English
 GlnSerProThrMetSerLeuTyrLys
 >
 Asundi
 New polynucleotide, useful for
neurodegenerative diseases.
 ADB48380 standard; cDNA; 2523
 21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
19-JUL-2000; 2000US-00620312.
 04-JAN-2002; 2002US-00037270
 Novel human cDNA SEQ ID NO
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 LIU C.
ASUNDI V.
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 WPI; 2003-678194/64.
 (ZHOU/) ZHOU P.
(TANG/) TANG Y T.
(LIUC/) LIU C.
(ASUN/) ASUNDI V.
 Percent Similarity:
Best Local Similarity:
 Tang YT,
 US2003104529-A1.
 Homo sapiens
 04-DEC-2003
 Alignment Scores:
 05-JUN-2003
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 Query Match:
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 | IleGlyLvsLysLysGlylleGlnGlyHisTyrAsnSerCysTyrLeuAspSerThrLeu
 ATTGGGAAGAAGGAAGCATCCAGGGTCATTACAATTCTTGTTACTTAGACTCAACCTTA
 PheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArgProLysGluLys
 TTCTGCTTATTTGCTTTTAGTTCTGTTCTGGACACTGTGTTACTTAGACCCCAAAGAAAAG
 AACGATGTAGAATTTATAGTGAAACCCAAGAGCTACTGAGGGACAGAAATTGTTAATTCCT
 LeukrgileTyrGlyTyrValCysAlaThrLysIleMetLysLeuArgLysIleLeuGlu
 CTGAGAATATATGGATATGTGTGTGCCCACAAAAATTATGAAACTGAGGAAAATACTTGAA
 LysValGluAlaAlaSerGlyPheThrSerGluGluLysAspProGluGluPheLeuAsn
 AAGGTGGAGCCTGCATCAGGATTTACCTCTGAAGAAAAAAGATCCTGAGGAATTCTTGAAT
 IleLeuPheHisHisIleLeuArgValGluProLeuLeuLysIleArgSerAlaGlyGln
 LysvalGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGluLysValGlyVal
 AAGGTACAAGATTGTTACTTCTATCAATTTTTTATGGAAAAAAAGAGAAAGTTGGCGTT
 ProThr11eGlnGlnLeuLeuGluTrpSerPhe11eAsnSerAsnLeuLysPheAlaGlu
 CCCACAATTCAGCAGTTGTTAGAATGGTCTTTTATCAACAGTAACCTGAAATTTGCAGAG
 Lys1lePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAspThrProArgGln
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Mon

1628 1748 1808 780 800 Human, oxidoreductase enzyme, transferase, hydrolase, lyase, isomerase, ligase, hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; CCCACAATTCAGCAGTTGTTAGAATGGTCTTTTATCAACAGTAACCTGAAATTTGCAGAG ProThr11eGlnGlnLeuLeuGluTrpSerPhe11eAsnSerAsnLeuLysPheAlaGlu Lys11ePheProSerLeuGluLeuAsn11eThrAspLeuLeuGluAspThrProArgGln GluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspAspSerAlaTrpLeuPhe GAAACAAGCCACTATGTTGCTTTTGTGAAGTATGGGAAGGACGATTCTGCCTGGCTCTTC PheaspSerWetalaaspargaspGlyGlyGlnasnGlyPheasnIleProGlnValThr CCATGCCCAGAAGTAGGAGAGAGATCTGAAAGATGTCTCTGGAAGACCTGCATTCCTTGGAC LysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGluLysValGlyVal AspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAlaValLeuCysIle TTTGACAGCATGGCCGATCGGGATGGTGGTCAGAATGGCTTCAACATTCCTCAAGTCACC ProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeuHisSerLeuAsp RESULT 10
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DE CDNA
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17-NOV - 2000; 2000US - 024921P

17-NOV - 2000; 200U
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 Homo sapiens
 02-AUG-2001
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PR 11-DEC-2000; 2000US-0259678P.

X (HUWA-) HUMAN GENOME SCI INC.

PA (HUWA-) HUMAN GENOME SCI INC.

R (Seen CA, Barash SC, Ruben SM;

X (Seen Call See ```

SQ Sequence 4716 BP; 1397 A; 848 C; 1036 G; 1431 T; 0 U; 4 Other.

Alignment Scores:

Pred. No.:

Score:

641.00

Matches:

668

Percent Similarity:

99.55\$

Mismatches:

Query Match:

67.54\$

Indens:

1 Gaps:

1 Gaps:

1 Gaps:

1 A

US-09-671-687A-3 (1-949) x AAS41617 (1-4716)

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|----|--|
| ò | 282 LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsnAspllellePro 301 |
| g | 212 CTTTGTAGTTTTGCGTGTGTTGAAGTACAATTCTATTGCACATCAATGATATCCCA 271 |
| È | 302 GluserValThrGlnGluArgArgProProLyBLeuAlaPheMetSerArgGlyValGly 321 |
| QQ | 272 GAGAGTGTGACGCAGGAAAGGAGGCCTCCCAAACTTGCCTTTATGTCAAGAGGTGTTGGG 331 |
| ò | 322 AsplyselySerSerHisAsnLysProLysAlaThrGlySerThrSerAspProGly 341 |
| οp | 332 GACAAAGGTTCATCCAGTCATAATAAACCAAAGGCTACAGGATCTACCTCAGACCCTGGA 391 |
| ò | 342 AsnArgArgSerGluLeuPheTyrThrLeuAsnGlySerSerValAspSerGlnPro 360 |
| qq | 392 AATAGAAACAGATCTGAATTATTTTATACCTTAAATGGGTCTTCTGTTGATGACCAACCA |
| Ġ | 361 GlnSerLygSerLygAsnThrTrpTyrIleAspGluValAlaGluAspProAlaLysSer 380 |
| Dp | 452 CAATCCAAATCAAAAATACATGGTACATTGATGAAGTTGCAGAAGACCCTGCAAAATT 511 |
| ò | 381 LeuThrGlulleSerThrAspPheAspArgSerSerProProLeuGlnProProVal 400 |
| qq | 512 CTTACAGAGATATCTACAGACTTTGACCGTTCTTCACCACCACCACCACCACCCTCCTCCTGTG 571 |
| ò | 401 AgnSerLeuThrThrGluAgnArgPheHisSerLeuProPheSerLeuThrLygMetPro 420 |
| | |

| Ор | 572 | AACTCACTGACCACCGAGAACAGATTCCACTCTTACCATTCAGTCTCACCAAGATGCCC 631 |
|----------------|------|---|
| δ | 421 | AsnThrasnGlySerIleGlyHisSerProLeuSerLeuSeralaGlnSerValMetGlu 440 |
| DÞ | 632 | AATACCAATGGAAGTATTGGCCACAGTCCACTTTCTCTGTCAGCCCAGTCTGTAATGGAA 691 |
| ζ | 441 | GluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetProProGlyAsnSer 460 |
| q <sub>Q</sub> | 692 | GAGCTAAAACACTGCACCCGTCCAAGAGAGTCCACCTTGGCCATGCCTCCTGGGAACTCA 751 |
| ò | 461 | |
| Dp | 752 | CATGGTCTAGAAGTGGGCTCATTGGCTGAAGTTAAGGAGAACCCTCTTTCTATGGGGTA 811 |
| Š | 481 | |
| du · | 812 | ATCCGTTGGATCGGTCACCACCAGGACTGAATGAAGTGCTCGCTGGACTGGAACTGGAA 871 |
| ο̈́λ | 501 | AspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyrPheThrCysAla 520 |
| Ор | 872 | GATGAGTGTGCAGGCTGTACGGATGGAACCTTCAGAGGCACTCGGTATTTCACCTGTGCC 931 |
| ò | 521 | LeulyslyshlaleuPheVallysLeulysSerCysArgFroAspSerArgPheAlaSer 540 |
| Op | 932 | crgaadaaddcccrdrrrcrdaaacrdaaddcrdcadccrdacrtcradgrrrdcarca 991 |
| ò | 541 | LeuGinProvalSerAsnGinIleGluArgCysAsnSerLeuAlaPheGlyGlyTyrLeu 560 |
| DP | 992 | TIGCAGCCGGTTTCCAATCAGATTGAGCGCTGTAACTCTTTAGCATTTGGAGGCTACTTA 1051 |
| ζō | 561 | SerGluValValGluGluAsnThrProProLysMetGluLysGluGlyLeuGluIleMet 580 |
| Db | 1052 | AGTGAAGTAGTAGAAGAAAATACTCCACCAAAAATGGAAAAAGGAGGTTGGAGATAATG |
| δ | 581 | leGlyLygLygLygGlyIleGlnGlyHisTyrAsnSerCysTyrLeuAspSerThrLeu 600 |
| qq | 1112 | ATTGGGAAGAAGGCATCCAGGGTCATTACAATTCTTGTTACTTAGACTCAACCTTA 1171 |
| ò | 601 | PheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArgProLysGluLys 620 |
| qq | 1172 | TTCTGCTTATTTGCTTTTAGTTCTGTTCTGACACTGTGTTACTTAGACCCAAAGAAAG |
| ò | 621 | AsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGluIleValAsnPro 640 |
| Ωp | 1232 | AACGATGTAGAATATTATAGTGAAACCCAAGAGCTACTGAGGACAGAAATTGTTAATCCT 1291 |
| 8 | 641 | LeuArgileTyrGlyTyrValCysAlaThrLysIleMetLysLeuArgLysIleLeuGlu 660 |
| qa | 1292 | CTGAGAATATATGGATATGTGTGTGCCACAAAATTATGAAACTGAGGAAAATACTTGAA 1351 |
| ολ | 661 | LysValGluAlaAlaSerGlyPheThrSerGluGluLysAspProGluGluPheLeuAsn 680 |
| qq | 1352 | AAGGTGGAGGTGCATCAGGATTTACCTCTGAAGAAAAGATCCTGAGGAATTCTTGAAT 1411 |
| δ | 681 | IleLeuPheHisHisIleLeuArgValGluProLeuLeuLysIleArgSerAlaGlyGln 700 |
| qq | 1412 | ATTCTGTTTCATCATATTTTAAGGGTAGAACCTTTGCTAAAAATAAGATCAGCAGGTCAA 1471 |
| δ | 701 | LysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGluLysValGlyVal 720 |
| qq | 1472 | AAGGTACAAGATIGTIACTICTAICAAATTITTATGGAAAAAAAAGAAGATGGCGTT 1531 |
| ò | 721 | ProThrileGinGlnLeuLeuGluTrpSerPheileAsnSerAsnLeuLysPheAlaGlu 740 |
| qa | 1532 | CCCACAATTCAGCAGTTGTTAGAATGGTCTTTTATCAACAGTAACCTGAAATTTGCAGAG 1591 |
| ò | 741 | AlaProSerCysLeullelleGlnMetProArgPheGlyLysAspPheLysLeuPheLys 760 |
| qa | 1592 | GCACCATCATGTTTTTTTTTTTTTTTTTTTTTTTTTTTT |
| ò | 761 | LysilePheProSerLeuGluLeuAsnileThrAspLeuLeuGluAspThrProArgGln 780 |
| qq | 1652 | TITICCTICTCTGGAATTAAATATAACAGATTTACTTGAAGACACTCCCAGACAG |

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largeth cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonuclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 complementary strand of a polynuclectide comprises one of the 5602 oligonuclectide sequences defined in the specification, where the oligonuclectide comprises at least 15 nuclectides; or (b) a combination of a polynuclectide which comprises a 5 -end complementary strand of a polynuclectide which comprises a 5 -end sequence and an oligonuclectide comprising a sequence complementary to a complementary strand of a polynuclectide which comprises a 5 -end sequence and an oligonuclectide comprises a 1 -end sequence complementary to a conjumnal confict sequence and sequence is selected from those defined in the configurally full-length comprises and the combination of the 5'-end sequence sets can be used in antisense therapy and in compensation. The primer sets can be used in antisense therapy and in comparisons. The primers are useful for synthesising polynuclectides, checking and comparisons of the abnormality of the proceins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and any specialised methods. AAH13633 to AAH13633 represent human amino acid sequences; and any the exemplification of the oligonuclectides. all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YThrVall1ePheCysAspValLeuProGlyLysGluSerLeuGlyTyrPheValGlyVa 265
                                                                                                    present invention describes primer sets for synthesising 5602 full-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspValValGluIleAsnGluLysPheThrGluLeuLeuLeuAlaIleThrAsnCysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGTTGTAGAGATAAATGAAAAGTTCACAGAGTTACTTTTGGCAATTACCAATTGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGAGGTTCAGCCTGTTTAAAAACAGAAACAGACTAAGTAAAAGGCCTCCAAATAGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyCysProValLysValGlnLeuArgSerGlyGluGluLysPheProGlyValValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCTGTCCTGTGAAAGTACAGCTGAGATCTGGGGAAGAAAAATTTCCTGGAGTTGTACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheArgGlyProLeuLeuAlaGluArgThrValSerGlyIlePhePheGlyValGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trcadaddaccccretradcadadadacadrcrcccdaararrcrrrddagrrdaarrd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuGluGluGluGlyArgGlyGlnGlyPheThrAspGlyValTyrGlnGlyLyPsGlnLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGAAGAAGGTCGTGGTCAAGGTTTCACTGACGGGGTGTACCAAGGGAAACAGCTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnCysAspGluAspCysGly---PheValAlaLeuAspLysLeuGluLeuIleGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGTGTGATGAAGATTGTGGTGTTTGTTGCATTGGACAAGCTAGAACTCATAGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspAspThrAlaLeuGluSerAspTyrAlaGlyProGlyAspThrMetGlnValGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATGACACTGCATTGGAAAGTGATTACGCAGGTCCTGGGGGACACAATGCAGGTCGAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProProLeuGlulleAsnSerArgValSerLeuLysGly-GlyGluThrIleGluSerGl
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                                                  Listing;
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Conservative:
Mismatches:
Indels:
                                               SEQ ID NO 18842; 2537pp + Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-671-687A-3 (1-949) x AAH18625 (1-2845)
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98.51%
98.51%
64.07%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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                                                    Claim 8;
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length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
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                       CysArg1leCysGlyGlyLyLeuAlaMetTyrGluCysArgGluCysTyrAspAspProAsp
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T, Wakamatsu
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27-AUG-1999; 99JP-0030253.
11-JAN-2000; 2000JP-00118776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to purified proteins and genes encoding them, that are involved in T cell activation (I) and has an amino acid deletion, substitution or addition in the amino acid sequences. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of autoimmune disease (rheumatoid arthritis, asthma, multiple solerosis and diabetes), allergic disease, infectious disease, AlDS, and acute or chronic rejection at organ transplant or bone marrow transplant. This sequence corresponds to a cDNA for a protein involved in T cell activation.
                                                                                                            se; gene; antiallergic; antiarthritic; antiasthmatic; antidiabetic; anti-HIV; antimicrobial; antirheumatic; immunosuppressive; neuroprotective; gene therapy; T cell activation; diagnosis; autoimmune disease; rheumatoid arthritis; asthma; multiple sclerosis; diabetes; allergic disease; infectious disease; AlDS; chronic rejection; organ; bone-marrow transplant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 allergic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New purified protein involved in T cell activation, useful for diagnosing, preventing and/or treating acquired immunodeficiency syndrome, autoimmune (e.g. rheumatoid arthritis, and diabetes), and infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T; 0 U; 0 Other;
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                                                                             cell activation associated cDNA #49
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243. .3113
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; 2002US-0436473P.
; 2003JP-00122113.
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2003US-0512846P
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28-APR-2003;
21-OCT-2003;
22-OCT-2003;
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Query Match:
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21 PheTyrLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLys 40

ATGAGTTCAGGCTTATGGAGCCAAGAAAAGTCACTTCACCCTACTGGGAAGAGCGGATT

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1322 GICTICIGITGACICACAACCACAATCCAAATCAAAAAAAACATGGTACATGATGAAGT

| RESULT 13 AAH18478 ID AAH18478 ID AAH18478 ID AAH18478 XX AC AAH18478; XX AC AAH18478; XX AC AAH18478; XX C AAH18478; XX C AAH18478; XX DE Human cDNA sequence SEQ ID NO:18586. XX C Homo sapiens. AAAAGAGGCTTGGAGATAATGTTGGGAAGAAGGCATCCAGGGTCATTACAATTC CV8TYLLeubspSerThrLeupheCysLeuphealapheSerSerValleubspThrVa TGTTACTTAGACTCAACCTTATTCTGCTTATTTGCTTTTAGTTCTGTTCTGGACACTGT LeuLeuargProLysGluLy8AsnAspValGluTyTYrSerGluThrGlnGluLeuLe |
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| ю | TTTAGCATTTGGGGGCTACTTAAGTGAAGTAGTAGAAGAAAATACTCCACCAAAATGGA uLysGluGlyLeuGlu1leMet1leGlyLysLysGlyIleGluGlyHisTykAsnSe |
| Qy 913 euGluAspLeuHisSerLeuAspSerArgArg1leGlnGlyC
 | rLeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGl |
| Qy 893 1yPheAsn11eProG1nVa1ThrProCysProG1uVa1G1yG3
 | ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSeGCTGAATTCAATTCAATTCAATTCAATTCAATTCAATTC |
| Qy 873 ysAspAspSerAlaTrpLeuPhePheAspSerMetAlaAspAa
 | YThrargTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysAr
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| Oy 853 lukeuPheAlaValkeuCysIleGluThrSerHisTyrValA] | Incutated to the second control of the secon |
| Qy 833 euDroLygAspleuDroAspIrpAspIrpArgHisGlyCysI. | Sectaince Interpretation of the section of the sect |
| Qy 813 yshsnThrGlnValHisLeuHisProLysArgLeuAsnHisLy | ualametProProGlyAsnSerHisGlyLeuGluValGlySerLeualaGluValLysGl 4 |
| Qy 793 rgGluCysTyrAspAspProAspIleSerAlaGlyLysIleLy | uSeraladinServalMetGludiuLeuAanThralaProvaldinGluSerProProLe 45
 |
| 773 euLeuGl

2581 TACTTGA | 413 OPheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLe 433
 |
| /33 1/1/18/18/18/18/18/18/18/18/18/18/18/18/ | 393 oProLeuGlnProProValAenSerLeuThrThrGluAenArgPheHisSerLeuPr 413
 |
| 753 lvīveāsenDheīveīen Dheīveīveī je Dheoresevīen | 1382 TGCAGAAGACCCTGCAAAATCTCTTACAGAGATATCTACAGACTTTGACCGTTCTCACC 1441 |

LysTyrAsnProValSerL 833 AlaPheValLysTyrGlyL 873 GluTyrLeuLysMetSerL 913 LeualametTyrGluCysa 793 LysGlnPheCysLysThrC 813 rapy; gene therapy; ss. K, Yamamoto J; rLeuTyrLys 949 |||||||||| TTTGTACAAA 3110

CCTTTGGAAATAAACTCCCAGAGTTTCTTTGAA-GGTTGGAGAAACAATAGAATCTGGAAC 479

421

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length

NO 18586; 2537pp + Sequence Listing; English SEQ ID 8 Claim The present invention describes primer sets for synthesising 5602 fulllength cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprises one of the 5602
complementary strand of a polynucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide so 1 selected from those defined in the
coligonucleotide which comprises at least 15 nucleotides and the combination of
coligonucleotide which cDNAs. The primers are also useful for the
coligonucleotide say specialised methods. AAH03166 to AAH13628 and
AAH13633 to AAH13633 to AAH3632 represent
coligonucleotides, all of which are used in the exemplification of the present invention

U; 0 Other; 0 G; 749 T; 562 ວ່ BP; 788 A; 470 Sequence 2569

eAspValGly ArgGlyProLeuLeuAlaGluArgThrValSerGlyIlePhePheGlyValGluLeuLeu GluGluGlyArgGlyGlnGlyPheThrAspGlyValTyrGlnGlyLysGlnLeuPheGln TGTGATGAAGATTGTGGCGTGTTTGTTGCATTGGACAAGCTAGAACTCATAGAAGATGT | ProLeuGlu11eAsnSerArgVa1SerLeuLyBGly-GlyGluThr11eGluSerGlyTh CysProValLysValGlnLeuArgSerGlyGluGluLysPheProGlyValValArgPhe TGTCCTGTGAAAGTACAGCTGAGATCTGGGGAAGAAAATTTCCTGGAGTTGTACGCTTC <u>AGAGGACCCCTGTTAGCAGAGAGACAGTCTCCGGAATATTCTTTGGAGTTGAATTGCTG</u> GAAGAAGGTCGTCGTCAAGGTTTCACTGACGGGGTGTACCAAGGGAAACAGCTTTTTCAG AspThrAlaLeuGluSerAspTyrAlaGlyProGlyAspThrMetGlnValGluLeuPro GACACTGCATTGGAAAGTGATTACGCAGGTCCTGGGGACACACATGCAGGTCGAACTTCCT AGGITICAGCCIGITITAAAAACAGAAACAGACIAAGIAAAAGGCCICCAAAIAGACGIGGGC CysAspGluAspCysGly---PheValAlaLeuAspLysLeuGluLeuIleGluAspAsp ArgPheSerLeuPheLysAsnArgAsnArgLeuSerLysGlyLeuGlnIl 2569 585 0 1 11 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: US-09-671-687A-3 (1-949) x AAH18478 (1-2569) 418.00 98.15% 98.15% 44.05% Percent Similarity: Best Local Similarity: Alignment Scores: 88 108 181 207 227 Н 128 121 148 301 61 168 241 188 361 Query Match: DB: ò q ò g ò ρp 8 6 8 6 S 8 8 ď

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1019 1199 1259 1379 1499 464 544 584 599 325 344 899 404 959 424 484 504 524 305 629 364 384 eAlaCysValGluSerThrIleLeuLeuHisIleAsnAspIleIleProGluSerValTh rGlnGluArgArgProProLysLeuAlaPheMetSerArgGlyValGlyAspLysGlySe GCAGGAAAGGAGGCCTCCCAAACTTGCCTTTATGTCAAGAGGTGTTGGGGACAAAGGTC ATCTGAATTATTTATACCTTAAATGGGTCTTCTGTTGACTCACACCACAACCAAATCCAAATC DMetAspasnProlleGlyAsnTrpAspGlyArgPheAspGlyVal---LeuCysSerPh CATGGATAACCCTATTGGCAACTGGGATGGAAGATTTGATGGAGTGCAGCTTTGTAGTTT TGCGTGTGTTGAAAGTACAATTCTATTGCACATCAATGATATCATCCCACAGAGAGTGTGAC rSerSerHisAsnLysProLysAlaThrGlySerThrSerAspProGlyAsnArg---Ar gSerGluLeuPheTyrThrLeuAsnGlySerSerValAspSerGlnProGlnSerLysSe eSerThrAspPheAspArgSerSerProProLeuGlnProProProValAsnSerLeuTh ySerIleGlyHisSerProLeuSerLeuSerAlaGlnSerValMetGluGluLeuAsnTh AAGTATTGGCCACAGTCCACTTTCTCTGTCACCCAGTCTGTAATGGAAGAGCTAAACAC CGGTCAGCCACCAGGACTGAATGAAGTGCTCGCTGGAACTGGAACTGGAAGATGATGTGC GCTGTTTGTGAAACTGAAGGCTGCAGGCCTGACTCTAGGTTTGCATTGCAGCCGGT TTCCAATCAGATTGAGCGCTGTAACTCTTTAGCATTTGGAGGCTACTTAAGTGAAGTAGT GAAAGGCATCCAGGGTCATTACAATTCTTGTTACTTAGACTCAACCTTATT rLysAsnThrTrpTyrIleAspGluValAlaGluAspProAlaLysSerLeuThrGluIl AGTGGGCTCATTGGCTGAAGTTAAGGAGAACCCTCCTTTCTATGGGGTAATCCGTTGGAT eGlyGlnProProGlyLeuAsnGluValLeuAlaGlyLeuGluLeuGluAspGluCysAl aGlyCysThrAspGlyThrPheArgGlyThrArgTyrPheThrCysAlaLeuLysLysAl aLeuPheValLysLeuLysSerCysArgProAspSerArgPheAlaSerLeuGlnProVa 1GluGluAsnThrProProLysMetGluLysGluGlyLeuGluIleMetIleGlyLysLy 8Ly8Gly11eGlnGlyHisTyrAsnSerCysTyrLeuAspSerThrLeuPheCysLeuPh uValGlySerLeuAlaGluValLysGluAsnProProPheTyrGlyValIleArgTrpIl 1SerAsnGlnIleGluArgCysAsnSerLeuAlaPheGlyGlyTyrLeuSerGluValVa rThrGluAsnArgPheHisSerLeuProPheSerLeuThrLysMetProAsnThrAsnGl rAlaProValGlnGluSerProProLeuAlaMetProProGlyAsnSerHisGlyLeuGl 480 540 099 780 840 096 424 444 1140 1200 504 1260 524 1320 544 564 1440 584 009 464 246 266 285 305 325 720 344 364 384 900 404 1020 484 1380 Ωp 요 셤 g g g d 셤 원 g a 셤 ద ò 셤 ŝ ò ò ò ò ò ò g ð à ò ð ð g 셤 8 ò ઠે ò ð

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Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral solerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer disgnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATGGTCTAGAAGTGGGCTCATTGGCTGAAGTTAAGGAGAACCCTCCTTTCTATGGGGTA 727
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                                                                                                                                                                       644
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
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2000US-00552317.
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2000US-00653450.
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2000US-00693036.
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P-PSDB; AAM41040.
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29-NOV-2000;
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25-APR-2000;
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB80441) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.

The nucleic acids, proteins, antibodies and (ant) agonists are useful in the disposis, treatment and prevention of: (a) cancer, e.g. breast and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune cancers e.g. Addison's dispesse, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, cardiovascular disorders such as myocardial isolatemias; (d) wound healing conditions. Or anaemia diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.
Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders.
                                                                                                               ATTCCTTGGACTCCAGGAGAATCCAAGGCTGTGCACGAAGACTGCTTTGTGATGCC
                                                                                 isSerLeuAspSerArgArg1leGlnGlyCysAlaArgArgLeuLeuCysAspAla
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P-PSDB; ABB89233.
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T cell activating gene
Patent: WO 2004058805-A 95 15-JUL-2004;
Asahi Kasei Pharma Corporation (JP)
Location/Qualifiers
1. 3302
/organism="Homo sapiens"
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Length:
Matches:
Conservative:
Mismatches:
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Alignment Scores: Pred. No.:

ORIGIN

(1-3302)US-09-671-687A-3 (1-949) x CQ834224

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| BC012342
Homo sapiens cylindromatosis
clone MGC:19923 IMAGE:4552767/
BC012342
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HOmo sapiens (human) | Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 3540) Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altechul, St. Zebebrg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Honding P. Jordan H. Morde T. Mark, S. Wagner, T. Wang, T. Heish F. | Distribenco, L., Marusina, R., Parmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P.P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wolley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., McKernan, R.J., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., G., Mangara, G., Man | Villalon, D.V., Muzily, D.C., Socialist, D.V., Buding, D.V., Muzily, D.C., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length | human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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2 (bases 1 to 3540)
Strausberg, R. | Direct Submission Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov | Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATC CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca | Steven Jones, Jennifer Asano, Ian Boadet, Varon Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzwinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Teai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra. | Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 29 Row: c Column: 5 This clone was Belected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14165257. | +<<<< |
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| RESULT 2 BC012342 LOCUS DCCUS DEFINITION ACCESSION VERSION KEYWORDS SOUNCE ORGANISM | REFERENCE
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REMARK | COMMENT | | PEATURES | |
| | | 676 uGluPheLeuAsnileLeuPheHisHisFileLeuArgValGluBroLeuLvsIleAr 696 | 716 uLysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLe 736 | 756 eLysLeuPheLysLysllePheProSerleuGluLeuAsnlleThraspLeuLeuGluas 776 | | | 856 aValleuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSe 876 | 896 eProGlnValThrProCysProGluValGlyGluTyrLeuLysNetSerLeuGluAspLe 916 | GCALICCIIGGACICCAGGAGACICCAGGAGACIGCAGGAGACIA
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   AAAGGCCTCCAAATAGACGTGGGCTGTCCTGTGAAAGTACAGCTGAGATCTGGGGAAGAA
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/db_xref = "LocualD: 1540"
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/db_xref = "MIM: 665018"
/db_xref = 
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//gene="CYLD"
//note="CAP_GIV; Region: CAP-GIV domain. CAP stands for cytoskeleton-associated proteins"
//db xref="CDD:pfam01302"
//gene="CYLD"
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Matches:
Conservative:
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                                                                                  'note="synonyms: CDMT, ('db_xref="LocusID:1540" 'db_xref="MIM:605018"
clone_lib="NIH MGC_46"
lab_host="DH10B-R"
roote="Vector: pOTB7"
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/gene="CYLD"
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Nagase_T., Ishikawa,K., Suyama,M., Kikuno,R., Hirosawa,M.,
Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
Prediction of the coding sequences of unidentified human genes.
XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
DNA Res. 5 (6), 355-364 (1998)
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Ohara,O., Suyama,M., Kikuno,R., Nagase,T. and Ishikawa,K.
Direct Submission
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Mammalia, Eutheria, Primates, Catarrhin, Hominidae, Homo.
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| . .5414
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<426. .3308
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Organiam="Homo sapiens"

/mol_type="mRNN"

/db xref="taxon:9606"

/clone="fh04363"
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| | RESULT 4 BD231207 LOCUS DEFINITION Human cytoskeleton associated proteins. ACCESSION BD231207.1 GI:33040977 KEYNORDS SOURCE Homo saplens (human) | ORGANISM Homo sapiens Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Matazoa; Chordata; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 4527) AUTHORS Lal,P., Tang,T.Y. Yue,H., Hillman,J.L., Bandman,O., Corley,N.C., Gueglar,K.J., Patterson,C., Azimzai,Y. and Baughn,M.R. TITLE Human cycoskeleton associated proteins JOURNAL Patent: JP 2002526076-A 9 20-AUG-2002; | INCYTE PHARMACEDITCALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002526076-A/9
PD 20-AUG-2002
PF 17-SEP-1999 JP 2000574254
PR 18-SEP-1998 US 60/172226,27-APR-1999 US 60/131321 PI
PREETI LAL, TOM Y TANG, HENRY YUE, JENNIFER L HILLMAN, OLGA PI
BANDMAN, | PI NELL COCKLEY, ARLD J GUEGLEK, CHANDRA FATIEKBON, IALDA AZIMZAI, PI MARIAH R BAUGHN PC CIZNIS/09, AGIK38/00, AGIR45/00, AGIP1/16, AGIP3/00, AGIP3/00, AGIP3/10, AGIP5/00, PC AGIP5/31, AGIP5/00, PC AGIP13/12, PC AGIP13/10, AGIP19/02, AGIP19/10, AGIP21/04, AGIP25/00, AGIP25/00, PC AGIP2/04, | PC A61P25/14, A61P25/16, A61P25/26, A61P21/04, A61P31/12, PC A61P31/18, A61P3 | CC Incyte ID No: 236332/ FH Key Location/Qualifiers FT Source 1.4527 FEATURES Location/Qualifiers FOORTH SOURCE 1.4527 FOORTH SOURCE 1. | Alignment Scores: Pred. No.: Score: Score: Percent Similarity: 98.44* Best Local Similarity: 98.44* Ouery Match: CS Core: CONSERVATIVE: 0 CONS | Qy 4 GlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgllePheTyrLeu 23 |
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| | UASDSBATTHTE-UPheCysLeuPheAlaPheSerSerValleuAspThrValleuLeuAr 616 | 636 ulleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuAr 656 | 676 uGluPheLeuAsnIleLeuPheHisHisIleLeuArgValGluProLeuLeuLysIleAr 696 | 16 ULy8ValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLe 736 | 756 eLysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAs 776 | 796 rAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGl 816 | 836 DieuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheal 856 | 896 eProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLe 916 |

| 1408 ATCTCTTACAGAGTTACAGACTTTGACCGTTCTTCACCACCACCCCCCCC | 99 yvalileArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGlyLeuGluLe 4 | 1888 ATCATTGCAGCCGGTTTCCAATCAGATTGAGCGCTGTAACTCTTTAGCATTTGGAGGCTA 1947 559 LEUSERGIUVAIVAIGIUGIUABATThr.ProproiysMetGluLysGluGlyLeuGluII 579 1948 CTTAAGTGAAGTAGAAGAAATACTCCACCAAAATGGAAAAAGAAGGCTTGGAGAT 2007 579 EMETILEGIYLYSLYSLYSGIYILEGINGIYHISTYRASNSERCYSTYKLEUASDSETTH 599 2008 AATGATTGGGAAGAAGAAGCATCCAGGGTCATTACAATTCTTACTTA | | 699 yGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGluLysValGl 719 2368 TCAAAAGTACAAGATTGTTACTTCTATCAAATTTTTATGGAAAAATGAGAAAGTTGG 2427 719 yValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeuLysPheAl 739 2428 CGTTCCCACAATTCAGCAGTTGTTACAACTTTTATCAACAGTAACCTGAAATTTGC 2487 739 aGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPheLysLeuPh 759 |
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us-09-671-687a-3.0ligo.rge

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ITNGERFSLFRONDRLDSTALESDDALSSDYAG
PGDTMQVBLPPLEINSRVSLKVGETIESGTVIFCDVLPGKESLGYFVGVDMDNPIGNW
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                                                                                                                                                                              /function="tumour suppressor/recessiv
/note="Familial Cylindromatosis Gene"
/codon_start=1
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organism="Homo sapiens"
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Submitted (29-NOV-1999) Stratton M.R., Cancer Genetics, Institute
of Cancer Research, 15 Cotswold Rd, Sutton,, Surrey. SM2 5NG.,
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                           TABABABATITITICCTTCTCTGGAATTABAATATAAACAGATTTACTTGAAGACACTCCCGG
                                                                                               gGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyrAspAspPr
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cyld gene; Familial Cylindromatosis.
Homo sapiens (human)
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 | 793 gGluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCy 81
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 | 833 uProLysAspLeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGl 8 | 853 uLeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLy 87 |
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GCTAC 14 | 334 rGlySerThrSerAspProGlyAsnArgArgSerGluLeuPheTyrThrLeuAsnGl 353
 | 353 ySerSerValAspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluVa 373 | 39 | 393 OPFOLEUGINPTOPTOPTOPTONALAGNSETLEUThTThrGluAsnArgPheHisSerLeuPr 413 | 413 OPheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLe 433
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LysGlyLeuGln11eAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
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Catarrhini; Hominidae; Homo.
GTTATTTGCTGTTCTCTGCGTAGGAAACAAGCCACTATGTTGTTTTGTGAAGTATGGGAA
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                                                                     sAspAspSerAlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGl
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/note="unnamed protein product"
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T cell activating gene
Patent: WO 2004058805-A 93 15-JUL-2004;
Asahi Kasei Pharma Corporation (JP)
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Mammalia; Eutheria; Primates;
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Length:
Matches:
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Mismatches:
Indels:
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Percent Similarity: Best Local Similarity: Query Match:

Alignment Scores: Pred. No.:

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US-09-671-687A-3 (1-949) x CQ834222

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rSerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVa 356

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| 135 MargarGlipProGliseriysSeriyabamThritpTyrilleAspGliuVallalaGliuS 376 1322 TGATCACACCAARTCCAARTCCAARTCCAARTCCAARCCAARTCCAARTCCAARCCAARCCAARTCCAARTCCAARCCAARCCAARTCCAARCAAR | |

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841 | 861 GluThtSerHieffyrValhlaPheValLysTyrGlyLysAspAspSsrAlaTrpLeuPhe | QY 941 GlnSerProThrMetSerLeuTyrLys 949 bb 2109 CAGAGTCCAACATGAGTTTGTACAAA 2135 RESULT 8 CQ719792 LOCUS CQ719792 DEFINITION Sequence 5726 from Patent W002068579. DNA linear PAT 03-FEB-2004 ACCESSION CQ719792 CQ719792 VERSION CQ719792.1 GI:42280649 |
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Homo sapiens (human)

Homo sapiens (human)

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Mammalia; Butheria; Primates; Catarrhini; Hominidae, Homo.

I (bases 1 to 2848)

Eliis, S. Sugiama, T., Wakamatsu, A., Magai, K., Saito, K., Yamamoto, J., Primer for synthesizing full-length cDNA and Otsuk, T.

Primer for synthesizing full-length cDNA and use thereof

Patent: JP 2002191363-A 15460 09-UUL-2002;

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OS Homo sapiens (human)

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PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU

PI SAITO,

PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI TRIICHI NAGAI, TETSUUI OTSUKI
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| OY 923 rglleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyrMetCysMetTyrGlnSerp 943 | REFERENCE 1 AUTHORS OLA,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishi,S., Sugiyama,T., Wakamateu,A., Nagai,K. and Oteuki,T. Ishi,S., Sugiyama,T., Wakamateu,A., Nagai,K. and Oteuki,T. Ishi,S., Sugiyama,T., Wakamateu,A., Nagai,K. and Oteuki,T. Finers for synthesising full-length cDNA and their use JOURNAL Pasociation for Biotechnology (JP) Research Association for Biotechnology (JP) Location/Qualifiers 1. 2845 Augustan Same "Homo sapiens" Amol type="unassigned DNA" Ab xref="unassigned DNA" Ab xref="unased protein product" Ab xref="unamed protein product" Acada product Ad Ab xreb Ad Ab | TSEENDEELLAINSCHOULENTIAL PHILINDELLAKIRSAGGNYOUGVETYOI PRINGER GGLAMYECREDELLAINSCHONGERIC GGLAMYECRECYDDPDISAGKIKGFCKTCNTGVHLHPKRITTDLLEDTPRGCRIC GGLAMYECRECYDDPDISAGKIKGFCKTCNTGVHLHPKRITTDLLEDTPRGCRIC GGLAMYECRECYDDPDISAGKIKGFCKTCNTGVHLHPKRINTNDVSLPKOLDDWDW RHGCIPCONNELFANLCTETSHTVAFTYGKGRODSANLFFDSNADDGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG |

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Isogai, T. and Otsuki, T.

Direct Submission

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Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

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sequencing: Research Association for Biotechnology; cDNA library
construction, 5' - & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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| 40 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly | 783 TACCAAGGGAAACAGCTTTTTCAGTGTGAAGATTGTGGCGTGTTTGTT | | | CATCAA
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ACTTGC | 314 aPhemetSerArgGlyValGlyAspLySGlySerSerSerHisAsnLySProLySAlaTh 334 | | 1 AladluAspProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerPr
 | 3 OProLeugInProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuDr
 | 13 oPheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSsrLe
 | 433 uSerAlaGlnSerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLe 453 | 453 uAlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLySG1 473
 | 473 uAsnProProPheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluVa 493
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| ThrAlaProValGlnGluSerProProLeuAlaMetProProGlyAsnSerHisGlyLeu 463
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                                                                                                                                                              SerSerSerHisAsnLysProLysAlaThrGlySerThrSerAspProGlyAsnArg--- 343
                                                                                                                                                                                      ArgSerGluLeuPheTyrThrLeuAsnGlySerSerValAspSerGlnProGlnSerLys 363
                                                                                                                                                                                                                                                                                   SerlysAsnThrTrpTyrIleAspGluValAlaGluAspProAlalysSerLeuThrGlu 383
                                                                                                                                                                                                                                                                                                                                                                                                                                           IleSerThrAspPheAspArgSerSerProProLeuGlnProProProValAsnSerLeu 403
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                                                                                                                                                                                                                                                                                                                                                                             ACCACCGAGAACAGATTCCACTCTTTACCATTCAGTCTCACCAAGATGCCCAATACCAT
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NEDO human cDNA sequenching project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
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HOMO Sapiens CDNA FLJ20180 fis, clone COL10238, highly similar to AR020656 Homo sapiens mRNA for KIAA0849 protein.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Sugano.S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
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| NCE 1 (bases 1) ORS Ota,T., Isogo 1 shii,S., Su E Primer for S Patent; JP 2 CO B HELIX RESEAR T OS HOMO SA PP 28-JUL-PP 28-JUL | Source 1.2569 | Qy 88 ValValGluIleAsnGluLy8PheThrGluLeuLeuLeuAlaIIeThrAsnCysGluGlu 107 | Qy 148 ArgGlyProLeuLeuAlaGluArgThrValSerGlyIlePheGlyValGluLeuLeu 167 Db 181 AGAGACCCCTGTTAGCAGACAGTCTCCGGAATATTCTTGGAGTTGCTG 240 Qy 168 GluGluGlyArgGlyGlnGlyPheThrAspGlyValTyrGlnGlyLysGlnLeuPheGln 187 Db 241 GAAGAGGTGTGGTGTTTGATTGATGAGGAGAGAGAGATTTTTT | Qy 207 AspThrAlaLeuGluSerAspTyrAlaGlyPrOGlyAspThrMetGlnValGluLeuPro 226 bb 361 GACACTGCATTGGAAAGTGATTACGCAGGTCCTGGGGACACATGCAGGTCGAACTTCCT 420 Cy 227 ProLeuGlulleAsnSerArgValSerLeuLySGly-GlyGluThrIleGluSerGlyTh 246 Db 421 CCTTTGGAAATAAACTCCAGAGTTCTTTGAA-GGTTGGAAACAATAGAATCTGGAAC 479 Cy 246 rValllePheCysAspValLeuProGlyLysGluSerLeuGlyTyrPheValGlyValAs 266 Cy 246 rValllePheCysAspValLeuProGlyLysGluSerLeuGlyTyrPheValGlyValAs 266 Chillillillillillillillillillillillillill |
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| 664 AlaAlaSerGlyPheThr-SerGluGluLyBABSpProGluGluPheLeuAsnIleLeuPh 1082 GCTGCATCAGGATTTGC-CTCTGAGAAAAGATCCTGAGGAATTCTTGAAAATTTCTGTT 683 eHisHIELEUASGATTTGC-CTCTGAGAAAAGATCCTGAGGAATTCTTGAATATTCTGTT CATCATATTTTAAGGGTAGAACCTTTGCTAAAAATAAGATCACAGGAATTCTTGATATTTTTTTT | Qy 763 | QY 843 GHisGlyCysIleProCysGlnAsnMetGluLeuPheAlaValLeuCysIleGluThrSe 863 Id IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | Qy 903 oGluValGlyCluTyrLeuLy8MetSerLeuGluAspLeuHisSerLeuAspSerArgAr 923 IB01 AGAAGTAGGAGAAGTACTTCGAAGATCTCTTGGACTCCTAGGACTCCTAGGACTCCAGGAG 1860 Qy 923 91leGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyrMetCysMetTyrGlnSerPr 943 Db 1861 AATCCAAGGCTGTGACAAGACTGCTTTGTGATGCATATATGTGCATGTACCAGAGTCC 1920 Qy 943 OThYMetSerLeuTyrLys 949 Db 1921 AACAATGAGATTGTACAAA 1939 | RESULT 14 BD160470 LOCUS LOCUS DEFINITION Primer for synthesizing full-length cDNA and use thereof. ACCESSION BD160470. G1:27666228 VERSION BD160470.1 G1:27666228 SURCESSION BD160470.1 G1:27666228 SOURCE Homo sapiens (human) ORGANISM Homo sapiens CRANISM Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammaila; Butheria; Primates; Catarrhini; Hominidae; Homo. |

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                                                                            rGlnGluArgArgProProLysLeuAlaPheMetSerArgGlyValGlyAspLysGlySe
                                                                                    AAAAAATACATGGTACATTGATGAAGTTGCAGAAGACCCCTGCAAAATCTCTTACAGAGAT
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                                                          recereretreaagracaarrerarrecacarcarcararcarceregagagrereac
                                                                                                                                                  gSerGluLeuPheTyrThrLeuAsnGlySerSerValAspSerGlnProGlnSerLysSe
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Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primers for synthesising full-length cDNA and their use

Location for Biotechnology (JP)

Research Association for Biotechnology (JP)

Location for Biotechnology (JP)

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                                         TGTCCTGTGAAAGTACAGCTGAGATCTGGGGAAGAAAATTTCCTGGAGTTGTACGCTTC
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420 | 246 Qy 584
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479 | 266 Oy 604
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| | 168 GluGluGlyArgGlyGlnGlyPheThraspGlyValTyrGlnGlyLysGlnLeuPheGln
 | 188 CysAspGluAspCysGlyPheValAlaLeuAspLysLeuGluLeuIleGluAspAsp
 | 207 ASpThrAlaLeuGluSerASpTyrAlaGlyProGlyAspThrMetGlnValGluLeuPro | 227 ProLeugluileAsnSerArgValSerLeuLysGly-GlyGluThrileGluSerGlyTh
 | 246 rvalilePheCysAspValLeuBroGlyLysGluSerLeuGlyTyrPheValGlyValAs
 | 266 pMetAspasnProlleGlyAsnTrpAspGlyArgPheAspGlyValLeuCysSerPh | 285 eAlaCysValGluSerThrIleLeuLeuHisIleAsnAspIleIleProGluSerValTh
 | 305 rGlnGluargArgProProLysLeuAlaPheMetSerArgGlyValGlyAspLysGlySe
 | 325 rSerSerHiabanLysProLysAlaThrGlySerThrSerAspProGlyBanArgAr
 | 344 gSerGluLeuPheTyrThrLeuAsnGlySerSerValAspSerGlnProGlnSerLysSe
 | 364 rLysabithrTrpTyrileAspGluValalaGluAspProalalysSerLeuThrGluil
 | 384 eSerThrAspPheAspArgSerSerProProLeuGlnProProProValAsnSerLeuTh | 404 rThrGludsnargPheHisSerLeuProPheSerLeuThrLysMetProAsnThrAsnGl | 424 ySerIleGlyHisSerProLeuSerLeuSerAlaGlnSerValMetGluGluLeuAsnTh
 | 444 rAlaProValGlnGluSerProProLeuAlaMetProProGlyAsnSerHisGlyLeuGl | 464 uValGlySerLeuAlaGluValLySGluAsnProProPheTyrGlyValIleArgTrpll | 484 eGlyGlnProProGlyLeuAsnGluValLeuAlaGlyLeuGluLeuGluAspGluCysAl | 504 aGlyCysThrAspGlyThrPheArgGlyThrArgTyrPheThrCysAlaLeuLysLysAl |

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| 1t Ouery 0. Score Match Length D 1 949 100 0 949 2 606 63.9 685 3 606 63.9 685 5 606 63.9 685 6 606 63.9 731 6 606 63.9 731 7 606 63.9 731 8 606 63.9 731 10 606 63.9 731 11 606 63.9 731 12 606 63.9 956 13 606 63.9 956 14 606 63.9 956 15 606 63.9 956 18 606 63.9 956 18 606 63.9 956 19 606 63.9 956 11 10 606 63.9 956 12 606 63.9 956 13 606 63.9 956 14 606 63.9 956 15 606 63.9 956 16 606 63.9 956 17 10 606 63.9 956 18 606 63.9 956 18 606 63.9 956 19 606 63.9 956 11 10 11.9 113 11 9 113 11 9 113 11 9 113 11 9 113 11 9 113 11 9 113 11 9 113 11 9 113 11 9 113 11 9 113 11 9 113 11 9 113 11 9 113 11 1 1 1 9 113 11 1 1 1 9 113 11 1 1 1 9 113 11 1 1 1 1 9 113 11 1 1 1 1 9 113 11 1 1 1 1 9 113 11 1 1 1 1 9 113 11 1 1 1 1 1 9 113 11 1 1 1 1 1 9 113 11 1 1 1 1 1 9 113 11 1 1 1 1 1 9 113 11 1 1 1 1 1 9 113 11 1 1 1 1 1 9 113 11 1 1 1 1 1 1 9 113 11 1 1 1 1 1 1 9 113 11 1 1 1 1 1 1 9 113 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | Description | 1 1 | Sequence 3, Appli | Seguence 2399, Ap | Semience 2399. Ap | Sequence 9, Appli | Sequence 9, Appli | Sequence 7, Appli | Sequence 1743, Ap | Seguence 1/43, Ap | Sequence 137, App. | Sequence 37570, A | Sequence 4, Appli | Sequence 4, Appli | Sequence 490, App | Segmence 490, App | Sequence 250, App | Sequence 250, App | Sequence 18843, A | ກ | | | Sequence 18587, A | Sequence 18587, A | Segmence 1207, Ap | Sequence 1609, Ap | Sequence 1609, Ap | Sequence 1609, Ap | Sequence 12393, A
Sequence 1610, Ap | Sequence 1610, Ap | Sequence 1610, Ap | Sequence 12400, A | Sequence 12395, A | Sequence 15308, A | Semience 27009, A | ີດ | , | <u>,</u> , | Sequence 11431, A
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902-12 | 450-16 | 450A-160 | 237-1609 | 827-1239
450-1610 | 450A-161 | 237-1610 | 827-1240 | 827-1239 | 827-1530 | 761-3467 | 993-2680 | 995-2114 | 997-1979 | 998-1143
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GENERAL INFORMATION:
APPLICANT: Hyseq inc.
TILE OF INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784FLPCT
CURRENT APPLICATION NUMBER: US/09/488,725A
CURRENT APPLICATION NUMBER: US/09/488,725A
CURRENT FILING DATE: 2000-12-22
PRIOR PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR PELICATION NUMBER: US/09/55,317
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR PLING DATE: 2000-07-19
PRIOR PLING DATE: 2000-07-19
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-10-19
PRIOR FILING DATE: 2000-10-19
PRIOR FILING DATE: 2000-10-19
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-10-19
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-10-19
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100.0%; Pred. No. 0;
ive 0; Mismatches
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us-09-671-687a-3.0ligo.rapm

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80 RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSL 139
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LNHKYNPVSLPKDLPDWDWRHGCIPCQNMELFAVLCIETSHYVAFVKYGKDDSAWLFFDS 883
                                                                                                                                                                                                                             MADRDGGONGFNIPQVTPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLLCDAYMCMYQSP 943
                                                                                                                                                                                                                                                                                                                                        ALFVKLKSCRPDSRFASLOPVSNOIBRCNSLAFGGYLSEVVBENTPPKMEKEGLEIMIGK 583
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                                                                                       PSLELNITDLLEDTPRQCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHPKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NOVEL NUCleic Acid and Polypeptides TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides FILE REFERENCE: 704FLPCT CURRENT APPLICATION NUMBER: US/10/286,897 CURRENT FILING DATE: 2002-11-01 PRIOR APPLICATION NUMBER: US/09/488,725 PRIOR PILING DATE: 2000-01-21 PRIOR PILING DATE: 2000-01-21 PRIOR PELICATION NUMBER: US/09/552,317 PRIOR APPLICATION NUMBER: US/09/598,042 PRIOR FILING DATE: 2000-06-20 PRIOR PILING DATE: 2000-07-19 PRIOR PILING DATE: 2000-07-19 PRIOR PILING DATE: 2000-07-19 PRIOR PILICATION NUMBER: US/09/62,191 PRIOR PILING DATE: 2000-09-14 PRIOR PILING DATE: 2000-09-14 PRIOR PILING DATE: 2000-09-14 PRIOR PILING DATE: 2000-10-19 PRIOR PILING DATE: 2000-10-19 PRIOR PILING DATE: 2000-10-19 PRIOR PILING DATE: 2000-11-29 NUMBER: US/09/693,036 PRIOR FILING DATE: 2000-11-29 NUMBER: US/09/693,036 NUMBER: US/0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2399, Application US/10286897; GENERAL INFORMATION:
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US-10-286-897-2399
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Best Local S
Matches 606
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                                                                                             620 MADRDGGQNGFNIPQVIPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLLCDAYMCMYQSP 679
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              560 LNHKYNPVSLPKDLPDWDWRHGCIPCQNMELFAVLCIETSHYVAFVKYGKDDSAWLFFDS 619
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                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hyseq Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784FLPCT
CURRENT APPLICATION NUMBER: US/10/258,898A
CURRENT FILING DATE: 2002-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIORENT FILING DATE: 2002-10-29
PRIOR PILING DATE: 2000-01-21
PRIOR PILING DATE: 2000-01-21
PRIOR PLING DATE: 2000-01-21
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-06-20
PRIOR PILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR PILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US09/662,191
PRIOR APPLICATION NUMBER: US09/662,191
PRIOR APPLICATION NUMBER: US09/693,036
PRIOR PILING DATE: 2000-10-19
PRIOR PILING DATE: 2000-10-19
PRIOR PILING DATE: 2000-10-19
PRIOR PILING DATE: 2000-10-19
PRIOR PILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7143
                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2399, Application US/10258898A; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT,
; ORGANISM: Homo sapiens
US-10-258-898A-2399
                                                                                                                                                                               TMSLYK 949
                                                                                                                                                                                                                                  680 TMSLYK 685
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US-10-258-898A-2399
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APPLICANT: TANG, Y. Tom
APPLICANT: TANG, Y. Tom
APPLICANT: TANG, Y. Tom
APPLICANT: HILLMAN, Jenry
APPLICANT: HILLMAN, Jenry
APPLICANT: GRELER, Neil C.
APPLICANT: GRELER, Karl J.
APPLICANT: GAIMER, Karl J.
APPLICANT: AZIMZAI, Yalda
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; OTHER INFORMATION: Incyte ID No: 2363327
US-10-921-707-9
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ORGANISM: Homo sapiens
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APPLICANT: TANG, Y. Tom
APPLICANT: TANG, Y. Tom
APPLICANT: YUE, Henry
APPLICANT: HILMAN, Jennifer L.
APPLICANT: HILMAN, Jennifer L.
APPLICANT: GUEGLE, Neil C.
APPLICANT: GUEGLE, Karl J.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BAUGHN, Mariah R.
TITLE OF INVENTION: HUMAN CYTOSKELETON ASSOCIATED PROTEINS FILE REFERENCE: PF-0594 PCT
CURRENT PPLICATION NUMBER: US/09/786,7978
CURRENT FILING DATE: 1998-09-18; 1998-09-18; 1999-04-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PERL PROGram
SEQ ID NO 9
LENGTH: 731
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US-09-786-7978-9
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ13PCT
CURRENT APPLICATION NUMBER: PCT/USO1/01239
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapp
SOFTWARE: PatentIn Vos: 2.0
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ORGANISM: Homo
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Sequence 7, Application US/60131321

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Lal, Preeti

APPLICANT: Hilman, Jennifer L.

APPLICANT: Hilman, Jennifer L.

APPLICANT: Baudman, Olga

APPLICANT: Baudman, Mariah R.

IITLE OF INVENTION: HUMAN CYTOSKELETAL PROTEINS

FILE REFERENCE: PP-0692 P

CURRENT FILING DATE: 1999-04-27

NUMBER OF SEQ ID NOS: 28

SEQ ID NO 7

LENGTH: 731

LENGTH: 731
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, OTHER INFORMATION: 2363327
US-60-131-321-7
 606; Conservative
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ORGANISM: Homo sapiens
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Sequence 137, Application PC/TUS0227777
Sequence 137, Application PC/TUS0227777
GENERAL INFORMATION:
APPLICANT: diabexus, Inc.
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
APPLICANT: Balceda, Susana
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
FILE REFERENCE: DEX-0346
FILE REPERIORS: DEX-0346
CURRENT APPLICATION NUMBER: PCT/US02/27777
CURRENT APPLICATION NUMBER: US 60/316,306
PRIOR APPLICATION NUMBER: US 60/316,306
NUMBER OF SEQ ID MOS: 170
SOFTWARE: Patentin version 3.1
                                                        ALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK 373
                                                                                                                                                                      YGYVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRVEPLLKIRSAGGKVO 493
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63.9%; Score 606; DB
Best Local Similarity 100.0%; Pred. No. 0;
Matches 606; Conservative 0; Mismatches
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PCT-US02-27777-137
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1743
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Pred. No. 0;
0; Mismatches 0;
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GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REPRENCE: PT213
CURRENT APPLICATION NUMBER: US/09/764,902
CURRENT PILING DATE: 2001-01-17
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100.0%; Pre
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; ORGANISM: Homo
US-09-764-902-1743
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Best Local S
Matches 606
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948 TMSLYK 953 | qq | 948 TMSLYK 953 |
| RESULT 11 PCT-USO2- Sequence APPLIC AUGREN AUMBER AUCHEN AUMBER AUCHEN AUMBER AUCHEN A | 13777A-137 1 Horomatic Composition PC/TUS0227777A ANT: diabeaus, inc. ANT: diabeaus, inc. ANT: Sul. Compositions and Methods related to Breast Specific Genes and Present Sul. Compositions and Methods related to Breast Specific Genes and Presents DEX-0346 ANT: Salceda, Susana OF INTENTION COMPOSITIONS ANT: Salceda, Susana OF INTENTION TO Compositions and Methods related to Breast Specific Genes and Presents DEX-0346 AT FILING DATE: 2002-10-24 APPLICATION NUMBER: PCT/US02/27777A FILING DATE: 2001-06-31 OF SEQ ID NOS: 170 OF SEQ ID NOS: 170 OF SEQ ID NOS: 170 ASS PATENTING DATE: 2001-06-31 ASS PATENTING DATE: 2001-06-31 ASS PATENTING DATE: 2001-06-31 ASS PATENTING SALPS AND | RESULT 12 US-10-170-2 Sequence Sequence GENERAL II FILE OF TITLE O | ### SERGING 1205E-37570 ### SERGING 1205E-37570 ### SERGING 205E-37570 ### |

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Sequence 4, Application US/09851673
GENERAL INFORMATION:
APPLICANT: Berry, Jonathan
APPLICANT: Fanslow, William
APPLICANT: Bougall, William
TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING
FILE REFRENCE: 3198
CURRENT APPLICATION NUMBER: US/09/851,673
CURRENT APPLICATION NUMBER: 2001-05-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 956
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SEQUENCE 4, APPLICATION:
GENERAL INFORMATION:
APPLICANT: IMMUNEX CORPORATION
APPLICANT: IMMUNEX CORPORATION
APPLICANT: Dougall, William C.
TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING
FILE REFERENCE: 3198-WO
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 09/851,673
PRIOR APPLICATION NUMBER: 09/851,673
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
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ORGANISM: Homo sapiens
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                 PSLELNI TDLLEDTPROCRI CGGLAMYECRECYDDPDI SAGKI KQFCKTCNTQVHLHPKR
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TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
TITLE OF INVENTION: PATHWAY
FILE REFERENCE: DO24 NP
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT PILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR APPLICATION NUMBER: U.S. 60/469,757
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PATENTING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PATENTING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PATENTING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
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DCYFYQIFMEKNEKVGVPT1QQLLEWSFINSNLKFAEAPSCLIIQMPRFGKDFKLFKKIF 770
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                                             LINHKYNPVSLPKDLPDWDWRHGCIPCQNMELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
                                                                                                                                                          MADRDGGQNGFNI PQVTPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLLCDAYMCMYQSP
                                                                                                                                                                          KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSBTQELLRTEIVNPLRI
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                                                                                           LNHKYNPVSLPKDLPDWDWRHGCIPCONMELFAVLCIETSHYVAFVKYGKDDSAWLFFDS
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100.0%; Pred. No. 0;
ive 0; Mismatches 0; Indels
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US-10-755-889-490
Sequence 490, Application US/10755889
GENERAL INFORMATION
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Best Local Similarity 100.
Matches 606; Conservative
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Sequence 4, Appli
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Sequence 116, App
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Sequence 116, App
Sequence 113, Ap
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Sequence 1133, Ap
Sequence 1643, Ap
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                                                                                                       , Search time 22 Seconds
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949,
1 MSSGLWSQEKVTSPYWEERI......RLLCDAYMCMYQSPTWSLYK 949
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1: /cgn2_6/ptodata/1/paa/NCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-60-655-875-144489
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US-10-472-963-633
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US-11-031-175-14754
PCT-US04-130-1133
PCT-US04-095.10-1133
PCT-US04-095.10-1133
PCT-US04-095.10-1134
US-11-027-843-4643
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US-11-028-457-4643
US-11-028-91-4643
US-11-028-458-4643
US-11-028-458-4643
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| 7 0.7 151 7 05-11-031-175-15459 Sequence 15459, A 7 0.7 151 7 05-11-079-463-6281 Sequence 6281, Ap 2 0.7 151 7 05-11-079-463-6281 Sequence 6281, Ap 2 0.7 151 8 05-60-655-875-154058 Sequence 154058, Ap 2 0.7 163 1 PCT-0852-3354-128 Sequence 128, App 2 0.7 163 7 05-11-080-997-1118 Sequence 128, App 2 0.7 165 8 05-60-655-875-131199 Sequence 128, App 2 0.7 165 8 05-60-655-875-131199 Sequence 131199, App 2 0.7 165 8 05-60-655-875-131199 Sequence 131199, App 2 0.7 165 8 05-60-655-875-131199 Sequence 169683, App 2 0.7 171 6 05-10-450-763-41951 Sequence 57655, Ap 2 0.7 171 6 05-10-450-763-57655 Sequence 2790, Ap 2 0.7 184 6 05-10-467-657-2790 Sequence 2790, Ap 2 0.7 184 6 05-10-467-657-2790 Sequence 2790, Ap | SULT 1 Sequence 4, Application US/10760678 Sequence 4, Application US/1076078 Septicant: Debts 1111am APPLICANT: Debts 1111am APPLICANT: Dougall, William APPLICANT: Dougall, William APPLICANT: Dougall, William APPLICANT: SCREENING ASSAYS FOR AGONISTS OF CD40 SIGNALING FILE REFERENCE: 3198 CURRENT APPLICATION NUMBER: US/10/760,678 CURRENT FILING DATE: 2001-05-08 NUMBER OF SEQ ID NOS: 4 SEQ ID NO 4 LENGTH: 956 TYPE: PRT ORGANISM: Homo sapiens -10-760-678-4 | Match 63.9%; Score 606; DB 6; Length 956;
Local Similarity 100.0%; Pred. No. 0;
Les 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | 344 RSELFYTLNGSSVDSQPQSKSKNYTWYIDEVAEDPAKSLTEISTDFDRSSSPLQPPPVNSL 403
 | 404 TTENRFHSLPFSLTKWPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPFGNSHGL 463
 | 464 EVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKK 523 | 524 ALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEIMIGK 583
 | 584 KKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRI 643
 | 644 YGYVCATKIMKLRKILEKVBAASGFTSEEKDPEFFLNILFHHILRVEPLLKIRSAGGKVQ 703
 | 161 VCAINTHALMANT LEANVEAGGE 1 SEEMULEER LINTER WILLIAM VEFULLANGAGEN V |
|---|--|--|---|--|--|--|--|--|---|
| | RESULT 1 US-10-760-678-4 ; SEQUENCE 4, A ; GENERAL INFOR ; APPLICANT: ; APPLICANT: ; APPLICANT: ; TITLE OF INV ; FILE REFEREN ; CURRENT FILI ; CURRENT APPL ; CURRENT PILING ; NUMBER OF SE ; SOFTWARE: PA ; SEQ ID NO 4 ; LENGTH: 956 ; TYPE: PRT ; ORGATH: 956 ; TYPE: PRT | Query Matc
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Matches 6 | \$ 95
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PCT-US04-26116-116
                                                                                                                                                                                                                                                          DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 633, Application US/10472963
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OP INVENTION: Human Secreted Proteins
FILE REFERENCE: PS954PCT
CURRENT APPLICATION WUMBER: US/10/472,963
CURRENT FILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: PCT/US02/09370
PRIOR APPLICATION NUMBER: US 60/278,650
PRIOR APPLICATION NUMBER: US 60/950,082
PRIOR APPLICATION NUMBER: US 60/950,082
PRIOR APPLICATION NUMBER: US 09/950,082
PRIOR APPLICATION NUMBER: US 09/950,083
PRIOR PILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 09/950,083
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100.0%; Pred. No. 30;
tive 0; Mismatches
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GENERAL INFORMATION:
APPLICANT: DYAX COTP.
TITLE OF INVENTION: TIEL-BINDING LIGANDS
FILE REFERENCE: 10280-083-001
CURRENT APPLICATION NUMBER: PCT/US04/26116
CURRENT APPLICATION NUMBER: US 60/494,713
PRIOR APPLICATION NUMBER: US 60/494,713
PRIOR FILING DATE: 2003-08-12
PRIOR FILING DATE: 2003-08-12
SOFTWARE: PSEC ID NOS: 161
SOFTWARE: PSEC DO NOS: 161
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Pred. No.
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                                                                                                                             TYPE: PRT; ORGANISM: Myxococcus xanthus US-11-031-175-12221
PRIOR FILING DATE: 2000-07-1
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 12221
LENGTH: 2216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 1834
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 100.
Matches 7; Conservative
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US-10-472-963-633
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Best Local Similarity
Matches 8; Conserv
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US-10-472-963-633
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LENGTH: 107
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                                                                                           711 DCYFYQIFMEKNEKVGVPTIQQLLEWSFINSNLKFAEAPSCLIIQMPRFGKDFKLFKKIF 770
                                                                                                                                                           PSLELNITDLLEDTPROCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHPKR 823
                                                                                                                                                                                                                                                                                     824 INHKYNPVSLPKDLPDWDWRHGCIPCONMELFAVLCIETSHYVAFVKYGKDDSAWLFFDS 883
                                                                                                                                                                                                                                                                                                                                                                                                                      MADRDGGQNGFNIPQVTPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLLCDAYMCMYQSP 943
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CURRENT APPLICATION NUMBER: US/60/655,875
CURRENT FILING DATE: 2005-02-24
NUMBER OF SEQ ID NOS: 171306
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
                                                                                                                                                                                                    HILL CONTROL OF THE C
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100.0%; Pred. No. 9.9;
1ve 0; Mismatches
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CURRENT FILING DATE: 2005-01-08
PRIOR APPLICATION NUMBER: 60/217,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 144489, Application US/60655875
GENERAL INFORMATION:
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100.0%; Pre-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCarter, James
Miller, Nancy
Williams, Deryck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guo, Liang
Kovalic, David
Lu, Maolong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    951 TMSLYK 956
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LENGTH: 190
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Sequence 330, Application PC/TUS0442360

GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation doing business as Massachusetts General APPLICANT: Hospital / Bayer AG
TITLE OF INVENTION: Nucleotide sequences involved in pain
FILE REFERENCE: 17633/2048
CURRENT APPLICATION NUMBER: PCT/US04/42360
CURRENT APPLICATION NUMBER: PCT/US04/42360
CURRENT APPLICATION NUMBER: 60/531,341
PRIOR FILING DATE: 19-Dec-2003
NUMBER OF SEQ ID NOS: 2587
SOFTWARE: Perl script
SEQ ID NO 330
INDICENTIAL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SOLAZYME, Inc.
APPLICANT: Dillon, Harrison F.
TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
TITLE OF INVENTION: Production
FILE REFERENCE: H2042101-CIP
CURRENT PAPLICATION NUMBER: PCT/USO5/01983
CURRENT FILING DATE: 2005-01-31
PRIOR FILING DATE: 2005-11-04
PRIOR FILING DATE: 2003-04-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OCCANISM: Rattus norvegicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Refseq / NP_062035
DATABASE ENTRY DATE: 2003-10-06
PCT-US04-42360-330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.7%; Score 7; DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
FORT-1805-01983-59
Sequence 59, Application PC/TUS0501983
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pre-
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      563 VVEENTP 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 VVEENTP 110
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            73 RSAGQKV 79
                                                                                                  PCT-US04-42360-330
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: History Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10 (15849)B
CURRENT APPLICATION NUMBER: US/11/031,175
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2005-07-10
NUMBER OF SEQ ID NOS: 16825
                                    Gaps
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                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 0.7%; Score 7; DB 6; Best Local Similarity 100.0%; Pred. No. 63; Matches 7; Conservative 0; Mismatches
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; OTHER INFORMATION: unsure at all Xaa locations US-11-031-175-14754
         Pred. No. 63;
100.0%; Preu. ...
                                                                                                                                                                                                                                                                             APPLICANT: Hufton, Simon E.
APPLICANT: Hufton, Simon E.
APPLICANT: Hoet, Rene
APPLICANT: Pieters, Henk
APPLICANT: Rockey, Kristen
TILE OF INVENTION: TIEL-BINDING LIGANDS
TILE REFERENCE: 10280-083001
CURRENT APPLICATION NUMBER: US/10/916,840
CURRENT FILING DATE: 2004-08-12
PRIOR PILING DATE: 2004-08-12
PRIOR FILING DATE: 2003-08-12
NUMBER OF SEQ ID NOS: 161
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 116
LENGTH: 107
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US-11-031-175-14754
; Sequence 14754, Application US/11031175
; GENERAL INFORMATION:
                                                                                                                                                                                                                                            Sequence 116, Application US/10916840 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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ORGANISM: Myxococcus xanthus
       Best Local Similarity 100.
Matches 7; Conservative
                                                                             429 SPLSLSA 435
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                                                                                                                        7 SPLSLSA 13
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                                                                                                                                                                                              RESULT 6
US-10-916-840-116
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JAPPLICANT: Doucette-Stamm, Lynn
APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Doucette-Stamm, Timochy
APPLICANT: Opperman, Timochy
APPLICANT: Houseweart, Chad Eric
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: DNUMBER: US/11/027,399
CURRENT APPLICATION NUMBER: US/10/640,833
PRIOR APPLICATION NUMBER: US 99/583,110
PRIOR APPLICATION NUMBER: US 99/583,110
PRIOR PILING DATE: 2000-05-26
PRIOR PELING DATE: 1998-06-30
PRIOR PILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR PILING DATE: 1997-07-02
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APPLICANT: Doucette-Stamm, Lynn
APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Cong. (Jandong
APPLICANT: Opperman, Timothy
APPLICANT: Opperman, Timothy
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
FILE REFERENCE: 3607.1000-024
CURRENT FILING DATE: 2003-08-14
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/081,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
THENCHALL OF THE SEQ ID NOS: 5322
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0.7%; Score 7; DB 7
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches
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; Sequence 4643, Application US/11027843
; GENERAL INFORMATION:
                                          Sequence 4643, Application US/11027399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptococcus pneumoniae US-11-027-399-4643
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LENGTH: 125
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APPLICANT: Livingston, Brian D.

APPLICANT: Sette, Alesandro

APPLICANT: S
APPLICANT: Cheanut, Robert W.
APPLICANT: Cheanut, Robert W.
APPLICANT: Cheanut, Mark J.
APPLICANT: Sette, Alesandro
APPLICANT: Newman, Mark J.
TITLE OF INVENTION: Methods of Identifying Optimal Variants of Peptide Epitopes
FILE REFERENCE: 2060.026PC01
CURRENT APPLICATION NUMBER: PCT/US04/09510
CURRENT FILING DATE: 2004-03-29
PRIOR PILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 1946
SOFTWARE: Patentin version 3.3
SEQ ID NO 1133
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NAME/KEY: misc_feature
LOCATION: (123)...(123)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature; LOCATION: (122)...(122)... OTHER INFORMATION: Xaa can be any naturally occurring amino acid PCT-USO4-09510-1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 122
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100.0%; Pred. No. 72;
tive 0; Mismatches
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100.0%; Pred. No. 71;
iive 0; Mismatches
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Best Local Similarity 100.
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Best Local Similarity
Matches 7; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 VELPPLE 78
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ORGANISM: Artificial
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DB 7; Length 125;
0.7%; Score 7;
Query Match
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Search completed: April 18, 2005, 09:57:31 Job time : 23 secs
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                                       LENGTH: 125
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US-11-028-169-4643

i Sequence 4643, Application US/11028169

i GENERAL INFORMATION:

i APPLICAMY: Doucette-Stamm, Lynn

APPLICAMY: Bush, David

i APPLICAMY: Dusperman, Timothy

i APPLICAMY: Deperman, Timothy

APPLICAMY: Deperman, Timothy

ITILE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

ITILE OF INVENTION: Number: US/11/028,169

CURRENT APPLICATION NUMBER: US/11/028,169

CURRENT APPLICATION NUMBER: US 10/640,833

PRIOR APPLICATION NUMBER: US 09/583,110

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 1998-06-30

PRIOR PELING DATE: 1998-06-30

PRIOR PELING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR PELING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR RELING DATE: 1997-07-02
                                                                                                                                                                                                                                                                                       Sequence 4643, Application US/11027878

| Sequence 4643, Application US/11027878
| Sequence 4643, Application US/11027878
| Sequence 4643, Application US/11027878
| PAPLICANT: Doucette-Stamm, Lynn
| APPLICANT: Bush, David
| APPLICANT: Bush, David
| APPLICANT: Coperman, Timothy
| APPLICANT: Coperman, Timothy
| APPLICANT: Opperman, Timothy
| APPLICANT: Opperman, Timothy
| TITLE OF INVENTION: Uncleic Acid and Amino Acid Sequences Relating to Streptococcus
| TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
| TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
| TITLE OF INVENTION: December 105/11/027,878
| CURRENT APPLICATION NUMBER: US/640,833
| PRIOR FILING DATE: 2003-08-14
| PRIOR FILING DATE: 2003-08-14
| PRIOR PLICATION NUMBER: US 69/107,433
| PRIOR FILING DATE: 1998-06-30
| PRIOR PLICATION NUMBER: US 66/085,131
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Best Local Similarity 100.0%; Pred. No. 73; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Streptococcus pneumoniae US-11-027-878-4643
                                                                                                688 RVEPLLK 694
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US-11-027-878-4643
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ORGANISM:
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                                                                               0.7%; Score 7; DB 7
100.0%; Pred. No. 73;
tive 0; Mismatches
                         ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-11-028-169-4643
                                                                              Query Match
Best Local Similarity 100.
Matches 7; Conservative
SEQ ID NO 4643
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OM protein

Run on:

Sequence:

Title:

Searched:

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APPLICANT: HILLMAN, Jennifer L.
APPLICANT: HILLMAN, Olga
APPLICANT: GENLEY, Neil C.
APPLICANT: GURLEY, Neil C.
APPLICANT: GURLEY, Neil C.
APPLICANT: GURLEY, Neil C.
APPLICANT: GURLEY, Narl J.
APPLICANT: ARTHRAI, Yalda
APPLICANT: ALTERSON, Chandra
APPLICANT: ALTERAL, Yalda
APPLICANT: ALTERAL, Yalda
APPLICANT: ALTERAL, Yalda
APPLICANT: ALTERAL, Yalda
APPLICANTON NUMBER: US/10/921,707
CURRENT FILING DATE: 2004-06-19
PRIOR APPLICATION NUMBER: US/09/786,797
PRIOR APPLICATION NUMBER: US/09/786,797
PRIOR APPLICATION NUMBER: US/09/786,797
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PERL PROGram
SEQ ID NO 9
LENGTH: 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 731;
US-10-437-963-188186
US-10-282-122A-60805
US-10-282-122A-60805
US-10-283-943-60805
US-09-983-802-607
US-09-973-276-150
US-10-632-706-154
US-10-632-706-154
US-10-081-872-219
US-10-081-872-219
US-10-081-872-219
US-10-88-205-73
US-10-88-205-73
US-10-424-599-266715
US-10-424-599-266715
US-10-437-963-195528
US-10-437-963-195528
US-10-437-963-162456
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; OTHER INFORMATION: Incyte ID No: 2363327
US-10-921-707-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/10921707
Publication No. US20050003447A1
GENERAL INFORMATION:
       LAL, Preeti
TANG, Y. Tom
YUE, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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       Sequence 4, Appli
Sequence 490, App
Sequence 250, App
Sequence 1609, Ap
Sequence 1610, Ap
Sequence 34675, A
Sequence 218, App
Sequence 218, App
Sequence 180681,
Sequence 180681,
Sequence 180681,
Sequence 180681,
Sequence 180681,
Sequence 180681,
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Sequence 4, Appli
                                                                                                                         April 18, 2005, 09:40:40; Search time 57 Seconds (without alignments) 5533.680 Million cell updates/sec
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1 MSSGLWSQEKVTSPYWEERI......RLLCDAYMCMYQSPTMSLYK 949
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(gnz 6/ptodata/1/pubpaa/US07 PUBCCMB.pep:*

(cgnz 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

(cgnz 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

(cgnz 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

(cgnz 6/ptodata/1/pubpaa/US08 PUBCCMB.pep:*

(cgnz 6/ptodata/1/pubpaa/US09 PUBCCMB.pep:*

(cgnz 6/ptodata/1/pubpaa/US09 NEW PUB.pep:*

(cgnz 6/ptodata/1/pubpaa/US09 NEW PUB.pep:*

(cgnz 6/ptodata/1/pubpaa/US09 NEW PUB.pep:*

(cgnz 6/ptodata/1/pubpaa/US10C PUBCCMB.pep:*

                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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0 US-981-673-4

6 US-10-755-889-49

6 US-10-788-792-250

5 US-10-264-237-1609

5 US-10-264-237-1609

1 US-09-864-761-34675

5 US-10-264-237-1610

1 US-09-864-761-34675

5 US-10-68-053A-218

6 US-10-838-226-218

6 US-10-437-963-180681

5 US-10-424-599-1150538

6 US-10-424-599-1150538
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                                                                                              - protein search, using sw model
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Maximum DB seq length: 2000000000
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Database :

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Sequence 6310, Ap Sequence 266715, Sequence 149557, Sequence 184451, Sequence 150683, Sequence 150683, Sequence 16228, Sequence 162456, Sequence 210307,

Sequence 83, Appl

Sequence 106579, Sequence 247009, Sequence 48578,

Sequence 237

Sequence

193894, 221399,

Sequence Sequence Sequence

276896

Sequence 154,

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Sequence Sequence

Sequence

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Sequence 490, Application US/10755889
Publication No. US20040171823A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
PATHWAY
TITLE OF INVENTION:
FILE REFERENCE: D0204 WORD
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT APPLICATION NUMBER: US. 60/440,068
PRIOR PELING DATE: 2004-01-13
PRIOR FILING DATE: 2003-01-14
PRIOR FILING DATE: 2003-01-14
PRIOR FILING DATE: 2003-01-14
PRIOR FILING DATE: 2003-01-14
PRIOR FILING DATE: 2003-05-12
 830
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                                                  TTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGL
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al Similarity 100.0%; Pred. No. 0;
606; Conservative 0; Mismatches
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 490
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ORGANISM: Homo sapiens
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Publication No. US20030165985A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Derry, William
APPLICANT: Panslow, William
APPLICANT: Bougall, William
APPLICANT: Bougall, William
APPLICANT: BOUGALL, William
APPLICANT: Panslow, William
APPLICANT: Dougall, William
APPLICANT: Dougall, William
APPLICANT: 1308
CURRENT APPLICATION NUMBER: US/09/851,673
CURRENT PILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
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100.0%; Pred. No. 0; tive 0; Mismatches
Best Local Similarity 100.
Matches 606; Conservative
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ORGANISM: Homo sapiens
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LOCATION: (209)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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COCATION: (227)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PAISIPI
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
FRIOR APPLICATION NUMBER: PCT/US01/16450
FRIOR PELLING DATE: 2001-05-19
FRIOR APPLICATION NUMBER: US 60/205,515
FRIOR APPLICATION NUMBER: US 60/205,515
FRIOR PILING DATE: 2000-05-19
SPRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOPTWARE: Patentin Ver. 3.1
SEQ ID NO 1609
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OTHER INFORMATION: Xaa
FEATURE:
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ORGANISM: Homo sapiens
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NAME/KEY: MISC_FEATURE
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NAME/KEY: MISC_FEATURE
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US-10-264-237-1609
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Publication No. US20040191819A1

GENERAL INFORMATION:
APPLICANT: Bayer Pharmaceuticals Corporation
APPLICANT: Breadeigh, Deepa
APPLICANT: Breadeigh, Deepa
APPLICANT: Breadeigh, Deepa
APPLICANT: Breadeigh, Despa
APPL
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; ORGANISM: Homo sapiens
US-10-788-792-250
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; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (257)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC FEATURE LOCATION: (187) COCATION: (187) OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids US-10-264-237-1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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                                                                                                                                                                                                                               653 MKLRKILBKVEAASGFTSEEKDPEEFLNILFHHILRVEPLLKIRSAGOKVODCYFYQIFM 712
                                                                                                                                                                                                                                                                                                                                                           61 EKNEKVGVPTIQQLLEWSFINSNLKFAEAPSCLIIQMPRFGKDFKLFKKIFPSLELNITD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 LLEDTPRQCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHPKRLNHKYNPVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      713 EKNEKVGVPTIQQLLEWSFINSNLKFAEAPSCLIIQMPRFGKDFKLFKKIFPSLELNITD 772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457 PGNSHGLEVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRY
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PAI3121
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
FRIOR APPLICATION NUMBER: PCT/US01/16450
FRIOR PILING DATE: 2001-05-18
FRIOR PILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFWRARE: PALENTIN VET: 3.1
SEQ ID NO 1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.6%; Score 148; DB 15; Length 238; 100.0%; Pred. No. 2.9e-137; cive 0; Mismatches 0; Indels
                                                                                                                                            Length 261;
                                                                                                                                                                                     0; Indels
                                                                                                                                       Query Match 21.9%; Score 208; DB 15; L
Best Local Similarity 100.0%; Pred. No. 1.5e-196;
Matches 208; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 LPKDLPDWDWRHGCIPCQNMELFAVLCI 208
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Matches 148; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC FEATURE LOCATION: (227)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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N: EXPRESSED IN FETAL LIVER, SIGNAL = 0.92

N: EXPRESSED IN HEL100, SIGNAL = 1.5

N: EXPRESSED IN HELA, SIGNAL = 1.3

N: EXPRESSED IN PLACENTA, SIGNAL = 1

N: EXPRESSED IN PLACENTA, SIGNAL = 1

N: EXPRESSED IN LUNG, SIGNAL = 1

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.3

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.3

N: EXPRESSED IN BRAIN, SIGNAL = 1.4

N: EXPRESSED IN BRAIN, SIGNAL = 1.4

N: EXPRESSED IN BRAIN, SIGNAL = 1.4
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 34675
                                               159 LEIMIGKKKGIQGHYNSCYLDSTLFCLF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR PELLING DATE: 2001-09-23
PRIOR PELLING DATE: 2000-02-04
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-36
PRIOR PELLING DATE: 2000-01-03
PRIOR PELLING DATE: 2000-01-04
PRIOR PELLING DATE: 2000-01-04
PRIOR PELLING DATE: 2000-01-03
PRIOR PELLING DATE: 2001-01-30
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PRIOR PELLING DATE: 2000-09-21
PRIOR PELLING DATE: 2000-09-21
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577 LEIMIGKKKGIQGHYNSCYLDSTLFCLF
                                                                                                                                                                                                                                                                  Sequence 34675, Application US/09864761
Patent No. US20020048763A1
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ORGANISM: Homo sapiens
FEATURE:
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  0.8%; Score 8; DB 14; Length 78;
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                                                                                                                                                                                                                                     Sequence 2.0. Application US/10838226

Publication No. US20040176278A1

GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Garrett, James E.
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Baldomero M.
TITLE OF INVENTION: B-Superfamily Conctoxins
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/838,226

CURRENT FILING DATE: 2004-05-05
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LOCATION: (1)..(122)
OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches
                100.0%; Prec. ...
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PRIOR APPLICATION NUMBER: US 10/058,053

PRIOR FILING DATE: 2000-01-29

PRIOR PILING DATE: 2010-01-29

NUMBER OF SEQ ID NOS: 340

SEQ ID NO 218

LENGTH: 78
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Ww. Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                    Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Conus terebra
                                                                   916 LHSLDSRR 923
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                                                                                                                           43 LHSLDSRR 50
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    Query Match
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cavalic David K
APPLICANT: Cavo Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: UMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 186263
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                                                                 Query Match 11.9%; Score 113; DB 9; Length 113; Best Local Similarity 100.0%; Pred. No. 5.9e-103; Matches 113; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: SWISSPROT HIT: Q03164, EVALUE 8.90e-01
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US-10-424-599-186263
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APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
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APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Water
CURRENT APPLICATION NUMBER: US/10/058,053A
CURRENT PILING DATE: 2002-07-05
PRIOR FILING DATE: 2001-01-29
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Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 340
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Conus terebra
US-10-058-053A-218
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ORGANISM: Glycine max
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Best Local Similarity
      ; OTHER INFORMALLY
US-09-864-761-34675
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LENGTH: 78
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APPLICANT: Barbazuk, Andery M. APPLICANT: Brad APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 188186
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
   0; Indels
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US-10-437-963-188186
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,727
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-66
PRIOR PILING DATE: 2000-05-66
PRIOR PLING DATE: 2000-09-06
   0; Mismatches
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; Publication No. US20040123343A1
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; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
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Forsyth, R.
   8; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carr, Grant
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                                                                     547 QIERCNSL 554
                                                                                                                                      120 QİERCNSL 127
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APPLICANT:
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   Matches
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US-10-424-599-170638
is Sequence 170638
sequence 170638
publication No. US20040031072A1
is GENERAL INFORMATION:
is APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei;
if TILE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
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TITLE OF INVENTION: Soy Nucleic Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molecules Acid Molec
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; Publication No. US20040031072A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Roya Thomas J
APPLICANT: La Tou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 159539
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                                                                                                  Query Match 0.8%; Score 8; DB 16; Length 122; Best Local Similarity 100.0%; Pred. No. 42; Matches 8; Conservative 0; Mismatches 0; Indele
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100.0%; Pred. No. 49;
.ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_125100C.1.pep. US-10-424-599-170638
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US-10-424-599-159539
; OTHER INFORMATION: Clone ID: PAT_MRT4530_78029C.1.pep
US-10-437-963-180681
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OTHER INFORMATION: ungure at all Xaa locations
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 VELLEEGR 171
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                                                                                                                                                                                                                                                                                                          16 SPPLAMPP 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Glycine max
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Best Local Similarity
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LOCATION: (1)..(1
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PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR PELICATION NUMBER: 60/253,625

PRIOR PELING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR PILING DATE: 2001-02-09

PRIOR PELING DATE: 2001-02-09

PRIOR PELING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-06

PRIOR FILIN
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312 SIGOYIOD 319
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Sequence:

Database :

Result

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Sequence 22217, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
FILE REPERBORCE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/094,190
FRIOR PILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22217
LENGTH: 228 ö 6077, Ap 381, App 4131, Ap Sequence 42367, Application US/09270767
Sequence 42367, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 42367
LENGTH: 344 Appli 44, App. 51839, Gaps Sequence Seq Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence 1 Sequence 4 Sequence 6 Sequence 3 Sequence 1 ö Length 228; Length 344; 0; Indels US-09-710-279-1222 US-09-270-767-33034 US-09-270-767-48251 US-09-270-767-48251 US-08-600-430-5 US-08-600-430-5 US-09-134-001C-4131 US-09-461-912A-44 US-09-711-164-381 US-09-711-164-381 US-09-711-164-381 US-09-513-999C-5797 US-09-513-999C-5797 US-09-513-3952-6627 US-09-107-433-3944 US-09-252-991A-17828 4, 0.8%; Score 8; DB 4 100.0%; Pred. No. 27; iive 0; Mismatches ALIGNMENTS

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APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZ010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
                                                                                                                                                                   CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER PILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER PILING DATE: 1997-07-08
EARLIER PILING DATE: 1997-07-08
EARLIER PILING DATE: 1997-07-08
EARLIER PILING DATE: 1997-07-08
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APPLICATION NUMBER: 60/052,803
TOTAL NATE: 1997-07-08
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PPLICATION NUMBER: 60/052,795
ILING DATE: 1997-07-08
PPLICATION NUMBER: 60/051,919
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FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,964
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PLICATION NUMBER: 60/051,920
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PLICATION NUMBER: 60/051,928
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APPLICATION NUMBER: 60/055,949
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APPLICATION NUMBER: 60/056,360
FILING DATE: 1997-08-18
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FILING DATE: 1997-07-08
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FILING DATE: 1997-07-08
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FILING DATE: 1997-07-08
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FILING DATE: 1997-07-08
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FILING DATE: 1997-08-18
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FILING DATE: 1997-08-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LING DATE:
                                                                                                                                                                                                                                                            Squence 20021, Application US/09252991A

Patent No. 655195
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
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APPLICANT: Goldman, Barry S.
APPLICANT: Slater, Stewen C.
APPLICANT: Slater, Stewen C.
APPLICANT: Slater, Stewen C.
APPLICANT: Midgand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPRENCE: 38-10(1584)B
FURRENT APPLICATION NUMBER: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 12221
                                                Gaps
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                                                Indels
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                        Pred. No. 39;
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0.8%; Score 8; DB 4
Best Local Similarity 100.0%; Pred. No. 2.1
Matches 8; Conservative 0; Mismatches
                                                Mismatches
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Pred. No.
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US-09-227-357-607
; Sequence 607, Application US/09227357
100.0%; Pre
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Best Local Similarity 100.0%; Pi
Matches 8; Conservative 0;
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ORGANISM: Pseudomonas aeruginosa
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                Best Local Similarity 100.
Matches 8; Conservative
                                                                                           225 LPPLEINS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 LNEVLAGL 273
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                                                                                                                                        164 LPPLEINS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           490 LNEVLAGL 497
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                                                                                                                                                                                                                                                 US-09-252-991A-20021
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49 AEAPSCL 55
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CLASSIFICATION:
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US-09-037-742B-24
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 SOFTWARE:
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i Sequence 6825, Application US/09513999C

j Patent No. 6783961

j APPLICANT: Dumas Milne Edwards, J.B.

j APPLICANT: Duclert, A.

j APPLICANT: Giordano, J.Y.

j TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

j PILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

j FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

j PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681
                                                                                                                                                                                 Gaps
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                                                                                                                                            Length 28;
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Batent No. 5770690
GENERAL INFORMATION:
APPLICANT: Bitler, Catherine Mastroni
APPLICANT: Bowersox, Stephen Scott
APPLICANT: Demo, Susan Dunham
APPLICANT: Demo, Susan Dunham
APPLICANT: Horne, William A.
APPLICANT: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: 27
CORRESPONDENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                            0.7%; Score 7; DB 3; 100.0%; Pred. No. 38;
                                                                                                                                                                               0; Mismatches
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100.0%; Pre
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
            SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 607
                                                                                                                                                           Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-999C-6825
                                                                                                                                                                                                                  732 INSNLKF 738
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NUMBER OF SEQ ID NOS:
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LENGTH: 56
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                                                                                                                                              Query Match
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Bax Omega Protein and Methods NUMBER OF SEQUENCES: 27 NUMBER OF SEQUENCES: ADDRESS: ADDRESSE: Deblinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,742B
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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100.0%; Pred. No. 79;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                               NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 5865-0017.30
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bitler, Catherine Mastroni
APPLICANT: Bowersox, Stephen Scott
APPLICANT: Crea, Roberto
APPLICANT: Demo, Susan Dunham
APPLICANT: Horne, William A.
APPLICANT: Zhou, Mei
                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/616,732A
FILING DATE: 15-MAR-1996
                                                                                     CLASSIFICATION: 514
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/495,042
ALTING DATE: 27-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/09037742B Patent No. 6140484
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 62 amino acida
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.7
Best Local Similarity 100.
Matches 7; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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US-09-513-999C-6103

i Sequence 6103, Application US/09513999C

i Bedent No. 6783961

i GENERAL INFORMATION:

APPLICANT: Duclert, A.

APPLICANT: Duclert, A.

TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION UNDBER: US/09/513,999C

CURRENT APPLICATION NUMBER: US 60/122,487

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR PILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOUTHWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Miegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10 (15849)
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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100.0%; Pred. No. 1.3e+02;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                       Length 62;
                                                                                                                                                                                                                                                                                                                                                    Query Match 0.7%; Score 7; DB 3; Best Local Similarity 100.0%; Pred. No. 79; Matches 7; Conservative 0; Mismatches
REFERENCE/DOCKET NUMBER: 5865-0017.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 14754, Application US/09902540; Patent No. 6833447; GENERAL INFORMATION:
                TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.7
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                         single
                                                                                                                                                                                                                                ANTI-SENSE: NO
CRIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
US-09-037-7428-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 PPLOPPP 106
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                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 AEAPSCL 55
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US-09-902-540-14754
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LENGTH: 108
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                                                                                                                                                                                                                              0.7%; Score 7; DB 4; Length 112;
100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08879995A
Patent No. 598506
GENERAL INFORMATION:
APPLICANT: Hillmen, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Kaser, Matthew R.
ITILE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Ler
                                                                                                                                                  IOCATION: (1)..(112)
COTHER INFORMATION: unsure at all Xaa locations US-09-902-540-14754
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: Herewith
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Best Local Similarity 100.0%; Pred. No.
Matches 7; Conservative 0; Mismatcl
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 Porter Drive
PRIOR FILING DATE: 2000-07-10
                                                                                              ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 116 amino acids
                NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 14754
LENGTH: 112
                                                                                                                                                                                                                            Query Match 0.7
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                          696 RSAGOKV 702
                                                                                                                                                                                                                                                                                                                                              73 RSAGOKV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                  NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-879-995A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-879-995A-4
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                                                                            TYPE: PRT
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Patent No. 6783961

GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT PAPLICANION NUMBER: US/09/513,999C
CURRENT PILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION DATE: 1999-02-26
                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                               0.7%; Score 7; DB 4; Length 125; 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: 91
; OTHER INFORMATION: Xaa-any one of the twenty amino acids
US-09-513-999C-4224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-09-107-433-2866
; Sequence 2866, Application US/09107433
; Patent No. 6800744
; Patent No. 680074710N:
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.7%; Score 7; DB 4
100.0%; Pred. No. 1.5
ive 0; Mismatches
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; NUMBER OF SEQ ID NOS: 5322
; LENGTH: 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: -23...1
OTHER INFORMATION: SCORE 4.1
OTHER INFORMATION: SEG LHILLILLEVAT/LD
                                                                                                                                                                                         ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa=Arg or Trp
                                                                                                                                                                                                                                               Query Match 0.7
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 4224
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Best Local Similarity 100.
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                            688 RVEPLLK 694
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112 RVEPLLK 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 LPGKESL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: UNSURE LOCATION: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-513-999C-4224
                                                                                                                                                                                                                US-09-583-110-4643
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Patent No. 6699703
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
CURRENT APPLICATION NUMBER: US/09/583,110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                   APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Raser, Matchew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
FILING DATE: US/09/215,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No. 1.4
tive 0; Mismatches
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF-0326 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,995
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, lucy J.
NAME: Billings, lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0326
                                                                                                                                   Sequence 4, Application US/09215096 Patent No. 6008194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 116 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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   563 VVEENTP 569
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                                                                                                                                                    Patent No. 6008194
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                          CITY: Pa.
STATE: CA
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                                                                                                                 US-09-215-096-4
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                           NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                              COUNTX: USER
TIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISOSGEO
COMPUTER: CUNKNOWN>
OCMPUTER: CUNKNOWN>
OCMPUTER: CUNKNOWN>
OCMPUTER: CUNKNOWN>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085131
FILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/061553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEFAX: (781)893-5007
TELEFAX: (781)893-5007
TELEFAX: (781)893-5007
TELEFAX: (781)893-5007
TELEFAX: (781)893-607
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: minoral acids
TYPE: TOTAL TYPE: DIOLEIN
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORIGINAL SOURCE:
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LOCATION: (B) LOCATION 1...134

SEQUENCE DESCRIPTION: SEQ ID NO: 2866:

US-09-107-433-2866
                                                                                                                                                        STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
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Search completed: April 18, 2005, 09:42:12 Job time : 58 secs

121 RVEPLLK 127

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